



CC may be used diagnosing of treating diseases or conditions associated with  
 CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,  
 CC heart disease, Jacobson Syndrome, Familial Nonchromaffin Paraganglioma,  
 CC Phenylketonuria and Charcot Marie Tooth disease

XX Sequence 215 AA;

Query Match 100.0%; Score 1125; DB 3; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYWRVCFVCEVPSSETBAVQGNPKLRICISCKREEVEATTVV 60  
 DB 1 MPAFNRLLPLASLVLIYWRVCFVCEVPSSETBAVQGNPKLRICISCKREEVEATTVV 60  
 QY 61 EMFYRPEGKDFLIYERNGHQEVESPPQGRLONNGSKDLODVSIITVNTLNDGSLTTC 120  
 DB 61 EMFYRPEGKDFLIYERNGHQEVESPPQGRLONNGSKDLODVSIITVNTLNDGSLTTC 120  
 QY 121 NVSRFEFEFAHRPPVKTTTRLPLRVTEBAGDFTSVSEIMMYILLVFLTMLFTLMTYC 180  
 DB 121 NVSRFEFEFAHRPPVKTTTRLPLRVTEBAGDFTSVSEIMMYILLVFLTMLFTLMTYC 180  
 QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVVEE 215  
 DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVVEE 215

#### RESULT 2

AAB50243  
 ID AAB50243 standard; protein; 215 AA.

AC AAB50243;

DE 13-MAR-2001 (first entry)

DE Rat sodium channel beta3 protein A1rxa94h5.

KM Rat; sodium channel beta3 protein; A1rxa94h5; pain; sleep disorder;  
 KM neurodegenerative disorder; mood disorder; muscle contraction.

OS Rattus sp.

PN WO200069912-A1.

XX 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US013144.

PR 14-MAY-1999; 99US-0134198P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Curtis RAJ;

XX WPI; 2001-122743/13.

DR N-PSDB; AAC90600.

PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal  
 PT root ganglion cDNA library for use in chromosome mapping, forensic  
 PT medicine, monitoring clinical trials and therapeutics.

XX Claim 9; Fig 2; 145PD; English.

XX The present invention provides the protein and coding sequences of the  
 CC rat sodium channel beta3 protein, designated A1rxa94h5. This protein is  
 CC involved in the generation of pain and other sensory or perceptible nerve  
 CC impulses, in the establishment and endurance of mood, neurodegenerative  
 CC and sleep disorders, and in the control of muscle contraction, including  
 CC movements such as the heartbeat, digestion and vascular tone. The  
 CC sequences can be used in predictive medicine, screening and diagnostic  
 CC assays, and in pharmacogenomics

SQ Sequence 215 AA;

Query Match 100.0%; Score 1125; DB 4; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYWRVCFVCEVPSSETBAVQGNPKLRICISCKREEVEATTVV 60  
 DB 1 MPAFNRLLPLASLVLIYWRVCFVCEVPSSETBAVQGNPKLRICISCKREEVEATTVV 60  
 QY 61 EMFYRPEGKDFLIYERNGHQEVESPPQGRLONNGSKDLODVSIITVNTLNDGSLTTC 120  
 DB 61 EMFYRPEGKDFLIYERNGHQEVESPPQGRLONNGSKDLODVSIITVNTLNDGSLTTC 120  
 QY 121 NVSRFEFEFAHRPPVKTTTRLPLRVTEBAGDFTSVSEIMMYILLVFLTMLFTLMTYC 180  
 DB 121 NVSRFEFEFAHRPPVKTTTRLPLRVTEBAGDFTSVSEIMMYILLVFLTMLFTLMTYC 180  
 QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVVEE 215  
 DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVVEE 215

#### RESULT 3

AAE35367  
 ID AAE35367 standard; protein; 215 AA.

AC AAE35367;

DE 17-JUN-2003 (first entry)

DE Rat sodium channel beta-3 subunit.

KM Rat; sodium channel beta-3 subunit; 98359 protein; gene therapy; AIDS;  
 KM shock; hypertension; psychiatric disease; obsessive-compulsive disorder;  
 KM bipolar affective disorder; attention deficit disorder; phobic disorder;  
 KM cardiovascular disorder; neurological disorder; spinocerebellar ataxia;  
 KM Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;  
 KM autoimmune disorder; cellular proliferative disorder; Krabbe's disease;  
 KM metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;  
 KM bone metabolism disorder; endothelial cell disorder; viral encephalitis;  
 KM acquired immune deficiency syndrome; peripheral neuropathy; arrhythmia;  
 KM poliomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;  
 KM dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;  
 KM pain.

OS Rattus norvegicus.

XX Key Location/Qualifiers

FT Domain 68..64

FT /note= "Conserved motif"

FT Domain 104..122

XX EPI258495-A1.

PD 20-NOV-2002.

PF 09-MAY-2002; 2002EP-00253262.

PR 09-MAY-2001; 2001US-0289893P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Curtis RAJ;

XX WPI; 2003-185859/19.

PT New isolated human sodium channel beta-4 subunit nucleic acid molecule  
 PT and polypeptide, useful for diagnosing and treating disorders with  
 PT aberrant beta-4 subunit function or expression, such as neurological and  
 PT cardiovascular diseases.

PS Disclosure; Page 56; 62pp; English.

XX  
CC The invention relates to human sodium channel beta-4 subunit, 98359  
CC polypeptides and polynucleotides. The methods and compositions of the  
CC invention are useful for diagnosing, screening and treating disorders  
CC associated with aberrant or deficient sodium channel beta-4 subunit  
CC function or expression such as paroxysmal nocturnal hemiparesis, hyperkalemic  
CC periodic paralysis, epilepsy, psychomotoric diseases (anxiety or phobic  
CC disorders, attention deficit disorder, obsessive-compulsive disorder and  
CC bipolar affective disorder), dementia, cardiovascular disorders  
CC (hypertension, shock, heart failure, arrhythmias and cardiomyopathy),  
CC neurological disorders (Alzheimer's or Parkinson's disease,  
CC spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders  
CC (diabetes, arthritis), cellular proliferative disorders (cancer), bone  
CC metabolism disorders, liver disorders, viral infections (AIDS, rabies,  
CC herpes simplex, poliomyelitis, viral encephalitis and peripheral  
CC neuropathy), endothelial cell disorders, demyelinating diseases (multiple  
CC sclerosis), pain and/or metabolic disorders (leukodystrophies, Krabbe's  
CC disease and Leigh disease). Polynucleotides of the invention are used to  
CC identify an individual from a biological sample (tissue typing), and in  
CC forensic identification of a biological sample. The invention is useful  
CC in gene therapy. The present sequence is rat sodium channel beta-3  
CC subunit. This sequence is used in the invention  
XX  
SQ Sequence 215 AA;

Query Match 100.0%; Score 1125; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.7e-99;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNLPLPLASIVLIYWRVCFVCEVPSSETEAVQGNPMKRCISCMKREVEATTVV 60  
DB 1 MPAFNLPLPLASIVLIYWRVCFVCEVPSSETEAVQGNPMKRCISCMKREVEATTVV 60  
QY 61 EMFYRPEGKDFLIYVRNGHOVESPPQGRLOMNSKDLQDVSTIVLNTLNDGLTYC 120  
DB 61 EMFYRPEGKDFLIYVRNGHOVESPPQGRLOMNSKDLQDVSTIVLNTLNDGLTYC 120  
QY 121 NVSRREFEFHRRFPVKTTRILPLRVTEAGEDFTSVSEIMYILVFLTLMLFIEMTYC 180  
DB 121 NVSRREFEFHRRFPVKTTRILPLRVTEAGEDFTSVSEIMYILVFLTLMLFIEMTYC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

#### RESULT 4

AAB36002 standard; protein; 215 AA.

XX  
AC AAB36002;  
XX  
DT 15-FEB-2001 (first entry)  
XX  
DE Human beta3 subunit.  
XX  
XX Human; beta sub-unit; beta3; analgesic; anticonvulsant;  
XX cerebroprotective; vasotrophic; cardiant; nootropic; cycostatic;  
XX dermatological; gene therapy; voltage-gated sodium channel; pain;  
XX epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;  
XX familial nonchromaffin paraganglioma; phenylketonuria;  
XX Charcot Marie Tooth disease.  
XX  
OS Homo sapiens.  
XX  
XX MO200063367-A1.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-FEB-2000; 2000WO-EP001783.  
XX  
PR 15-APR-1999; 99US-0129473P.

XX  
PA (WARR) WARNER LAMBERT CO.  
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
XX  
PI Cox P, Dixon A, Jackson A, Morgan K;  
XX  
DR WPI; 2000-665241/64.  
DR N-PSDB; AAC67837.

XX  
PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium  
XX channel, and their corresponding polypeptides, useful for detecting and  
XX treating sodium channel-associated conditions, e.g. pain, epilepsy and  
XX stroke.

PS Claim 34; Fig 4; 88pp; English.

XX  
XX The present sequence is given in the claims of a specification relating  
XX to a novel family of beta sub-unit proteins from a voltage-gated sodium  
XX channel. Human and rat beta sub-units, which have been collectively  
XX identified as beta3, have been isolated. The polynucleotides and  
XX polypeptides are useful for screening for agonists and antagonists of  
XX sodium channels. The agonists, antagonists, proteins and nucleic acids  
XX may be used for diagnosing or treating diseases or conditions associated with  
XX voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,  
XX heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,  
XX Phenylketonuria and Charcot Marie Tooth disease  
XX

SQ Sequence 215 AA;

Query Match 98.2%; Score 1105; DB 3; Length 215;  
Best Local Similarity 98.1%; Pred. No. 1.4e-97;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAFNLPLPLASIVLIYWRVCFVCEVPSSETEAVQGNPMKRCISCMKREVEATTVV 60  
DB 1 MPAFNLPLPLASIVLIYWRVCFVCEVPSSETEAVQGNPMKRCISCMKREVEATTVV 60  
QY 61 EMFYRPEGKDFLIYVRNGHOVESPPQGRLOMNSKDLQDVSTIVLNTLNDGLTYC 120  
DB 61 EMFYRPEGKDFLIYVRNGHOVESPPQGRLOMNSKDLQDVSTIVLNTLNDGLTYC 120  
QY 121 NVSRREFEFHRRFPVKTTRILPLRVTEAGEDFTSVSEIMYILVFLTLMLFIEMTYC 180  
DB 121 NVSRREFEFHRRFPVKTTRILPLRVTEAGEDFTSVSEIMYILVFLTLMLFIEMTYC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

#### RESULT 5

AAB85206 standard; protein; 215 AA.

XX  
AC AAB85206;  
XX  
DT 07-SEP-2001 (first entry)  
XX  
DE Human novel sodium channel beta1-like subunit.  
XX  
XX Sodium channel; sensory neurone specific channel; beta1-like subunit;  
XX SNS; therapeutic; pain; analgesic.  
XX  
OS Homo sapiens.  
XX  
XX Key  
XX FT 38, 122  
XX FT Domain /note="immunoglobulin domain"  
XX FT 157, 176  
XX FT Domain /note="transmembrane domain"  
XX  
XX MO200144293-A2.

PD 21-JUN-2001.  
XX  
XX 14-DEC-2000; 2000WO-GB004802.  
XX  
XX 17-DEC-1999; 99GB-00029970.  
XX  
XX (GLAXO ) GLAXO GROUP LTD.  
XX  
XX Plunpton M, Powell AJ, Saneau P;  
XX  
XX WPI: 2001-398129/42.  
XX  
XX N-PSDB; AAF84146.  
XX  
XX Novel sub-unit for voltage-gated sodium channel proteins for producing  
XX agents useful for treating pain.  
XX  
XX Claim 1; Fig 2; 31pp; English.  
XX  
XX The invention provides a novel beta1-like sub-unit for voltage-gated  
XX sodium ion channel polypeptide, specifically a sensory neurone specific  
XX channel (SNS) subunit. The novel beta1-like subunit is useful for  
XX producing a therapeutic agent which is useful treating pain in a patient.  
XX The subunit can be expressed by standard recombinant methodology. The  
XX present sequence represents a human novel sodium channel beta1-like  
XX subunit  
XX  
XX Sequence 215 AA;  
XX  
XX

Query Match 98.2%; Score 1105; DB 4; Length 215;  
Best Local Similarity 98.1%; Pred. No. 1.4e-97;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAPRLPLASLVLIYWRVCFPCVCEVSETEAVQGNPKLRICISCKREEVEATTIV 60  
DB 1 MPAPRLPLASLVLIYWRVCFPCVCEVSETEAVQGNPKLRICISCKREEVEATTIV 60  
QY 61 EMFYRPEGKDFLIYERNQHOEVESPFQGRLOMNGSKDLDVSIITVAVNTLNDGLTYC 120  
DB 61 EMFYRPEGKDFLIYERNQHOEVESPFQGRLOMNGSKDLDVSIITVAVNTLNDGLTYC 120  
QY 121 NVSRREFEFAHRRPFVKTRRLPLRVTGEAGDFTSVSEIMWYILLVFLTMLFIEMIYC 180  
DB 121 NVSRREFEFAHRRPFVKTRRLPLRVTGEAGDFTSVSEIMWYILLVFLTMLFIEMIYC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 6  
ABB05689  
ID ABB05689 standard; protein; 215 AA.  
XX  
XX ABB05689;  
XX

DT 30-APR-2002 (first entry)  
XX  
XX Human signal transduction protein clone amy2\_2f18.  
XX  
XX Human, foetal brain; foetal kidney; melanoma; testis; amygdala;  
XX gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX WO200198454-A2.  
XX  
XX 27-DEC-2001.  
XX  
XX 25-APR-2001; 2001WO-IB002050.  
XX  
XX 25-APR-2000; 2000US-0199380P.  
XX  
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.  
XX  
XX

XX  
XX Wiemann S;  
XX  
XX WPI: 2002-055860/07.  
XX  
XX N-PSDB; ABA93727.  
XX  
XX Human cDNA sequences and clones derived from human fetal brain, fetal  
XX kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic  
XX screening and therapy.  
XX  
XX Claim 1; Page 176; 611pp; English.  
XX  
XX

XX The present invention describes assemblages and computer readable media  
XX comprising novel human cDNA sequences and clones derived from human  
XX foetal brain, foetal kidney, melanoma, testis and amygdala cDNA  
XX libraries. ABA93702 to ABA93766 represent human cDNA sequences from the  
XX present invention which encode the proteins given in ABB05662 to  
XX ABB05729. The human cDNA sequences and clones can be used in gene  
XX therapy. The clones may be used in a variety of applications, for example  
XX they may be used in profiling assays, for providing large arrays of human  
XX genetic material for implementing large-scale screening strategies and  
XX for treating diseases via gene therapy procedures  
XX  
XX Sequence 215 AA;  
XX

Query Match 98.2%; Score 1105; DB 5; Length 215;  
Best Local Similarity 98.1%; Pred. No. 1.4e-97;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAPRLPLASLVLIYWRVCFPCVCEVSETEAVQGNPKLRICISCKREEVEATTIV 60  
DB 1 MPAPRLPLASLVLIYWRVCFPCVCEVSETEAVQGNPKLRICISCKREEVEATTIV 60  
QY 61 EMFYRPEGKDFLIYERNQHOEVESPFQGRLOMNGSKDLDVSIITVAVNTLNDGLTYC 120  
DB 61 EMFYRPEGKDFLIYERNQHOEVESPFQGRLOMNGSKDLDVSIITVAVNTLNDGLTYC 120  
QY 121 NVSRREFEFAHRRPFVKTRRLPLRVTGEAGDFTSVSEIMWYILLVFLTMLFIEMIYC 180  
DB 121 NVSRREFEFAHRRPFVKTRRLPLRVTGEAGDFTSVSEIMWYILLVFLTMLFIEMIYC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 7  
AAE35366  
ID AAE35366 standard; protein; 215 AA.  
XX  
XX AAE35366;  
XX

DT 17-JUN-2003 (first entry)  
XX  
XX Human sodium channel beta-3 subunit.  
XX  
XX Human, sodium channel beta-3 subunit; 98359 protein; gene therapy; AIDS;  
XX shock; hypertension; psychiatric disease; obsessive-compulsive disorder;  
XX bipolar affective disorder; attention deficit disorder; phobic disorder;  
XX cardiovascular disorder; neurological disorder; spinocerebellar ataxia;  
XX Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;  
XX autoimmune disorder; cellular proliferative disorder; Krabbe's disease;  
XX metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;  
XX bone metabolism disorder; endothelial cell disorder; viral encephalitis;  
XX acquired immune deficiency syndrome; peripheral neuropathy; arrhythmia;  
XX poliomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;  
XX dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;  
XX pain.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX Domain 38..70  
XX  
XX



FT /note= "Conserved motif"  
FT Domain 104, .122  
FT /note= "Conserved motif"  
XX EPI258495-A1.  
XX  
XX 20-NOV-2002.  
XX  
XX 09-MAY-2002; 2002EP-00253362.  
XX  
XX 09-MAY-2001; 2001US-0289893P.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Curtis RAJ;  
XX  
XX WPI; 2003-185859/19.  
XX  
XX New isolated human sodium channel beta-4 subunit nucleic acid molecule  
XX and polypeptide, useful for diagnosing and treating disorders with  
XX aberrant beta-4 subunit function or expression, such as neurological and  
XX cardiovascular diseases.  
XX  
XX Disclosure; Page 55-56; 62pp; English.  
XX  
XX The invention relates to human sodium channel beta-4 subunit, 98359  
XX polypeptides and polynucleotides. The methods and compositions of the  
XX invention are useful for diagnosing, screening and treating disorders  
XX associated with aberrant or deficient sodium channel beta-4 subunit  
XX function or expression such as paroxysmal congenital, hyperkalemic  
XX periodic paralysis, epilepsy, psychiatric diseases (anxiety or phobic  
XX disorders, attention deficit disorder, obsessive-compulsive disorder and  
XX bipolar affective disorder), dementia, cardiovascular disorders  
XX (hypertension, shock, heart failure, arrhythmias and cardiomyopathy),  
XX neurological disorders (Alzheimer's or Parkinson's disease,  
XX spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders  
XX (diabetes, arthritis), cellular proliferative disorders (cancer), bone  
XX metabolism disorders, liver disorders, viral infections (AIDS, rabies,  
XX herpes simplex, poliomyelitis, viral encephalitis and peripheral  
XX neuropathy), endothelial cell disorders, demyelinating diseases (multiple  
XX sclerosis), pain and/or metabolic disorders (leukodystrophies, Krabbe's  
XX disease and Leigh disease). Polynucleotides of the invention are used to  
XX identify an individual from a biological sample (tissue typing), and in  
XX forensic identification of a biological sample. The invention is useful  
XX in gene therapy. The present sequence is human sodium channel beta-3  
XX subunit. This sequence is used in the invention  
XX  
SQ Sequence 215 AA;  
Query Match 98.2%; Score 1105; DB 6; Length 215;  
Best Local Similarity 98.1%; Pred. No. 1,4e-97;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MPAFNLLPLASIVLVLYWVCPVCEVSETEAVQGNPMKLRCSCKMREVEATTVV 60  
DB 1 MPAFNLLPLASIVLVLYWVCPVCEVSETEAVQGNPMKLRCSCKMREVEATTVV 60  
QY 61 EWFYREGGKDFLIYERYNGHGVESPPQGRLOMNGSKDLQDVSTIVLVNTLNDGSLYTC 120  
DB 61 EWFYREGGKDFLIYERYNGHGVESPPQGRLOMNGSKDLQDVSTIVLVNTLNDGSLYTC 120  
QY 121 NVSREFEFEHAPFVVTTLIPLRVTEAGDEFTSVSSIMTYILLVFLTLMIEMTYC 180  
DB 121 NVSREFEFEHAPFVVTTLIPLRVTEAGDEFTSVSSIMTYILLVFLTLMIEMTYC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
RESULT 8  
ABR83183  
ID ABR83183 standard; protein; 215 AA.

XX  
XX ABR83183;  
XX 15-JAN-2004 (first entry)  
XX  
XX Human SCN3B protein.  
XX  
XX SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;  
XX neuroprotective; anesthetic; cycostatic; cerebroprotective; cardiant;  
XX hypotensive; gene therapy; SCN3B; human.  
XX  
XX Homo sapiens.  
XX  
XX W02003072751-A2.  
XX  
XX 04-SEP-2003.  
XX  
XX 25-FEB-2003; 2003WO-US006010.  
XX  
XX 25-FEB-2002; 2002US-0359382P.  
XX  
XX (UYVA-) UNIV VANDERBILT.  
XX  
XX George AL, Lossin C;  
XX  
XX WPI; 2003-712725/67.  
XX  
XX N-PDB; ACF57870.  
XX  
XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in  
XX screening for modulators, for treating e.g. epilepsy.  
XX  
XX Disclosure; Page 145-147; 176pp; English.  
XX  
XX The invention relates to a recombinantly expressed and isolated human  
XX SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally  
XX incorporated into a cell, is used to screen for specific modulators,  
XX potentially useful as anticonvulsant, antiepileptic, neuroprotective,  
XX analgesic and/or anesthetic agents, e.g. for treating severe myoclonic  
XX epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,  
XX motor endplate diseases, hypertension, congestive heart failure and  
XX muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic  
XX and metastatic cancer cell lines). These activities can also be provided  
XX by gene therapy vectors that express (I) or the modulators. The  
XX modulators, also antibodies directed against (I), are used to detect  
XX sodium channel polypeptides. The present sequence represents a human  
XX SCN3B protein  
XX  
SQ Sequence 215 AA;  
Query Match 98.2%; Score 1105; DB 7; Length 215;  
Best Local Similarity 98.1%; Pred. No. 1,4e-97;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MPAFNLLPLASIVLVLYWVCPVCEVSETEAVQGNPMKLRCSCKMREVEATTVV 60  
DB 1 MPAFNLLPLASIVLVLYWVCPVCEVSETEAVQGNPMKLRCSCKMREVEATTVV 60  
QY 61 EWFYREGGKDFLIYERYNGHGVESPPQGRLOMNGSKDLQDVSTIVLVNTLNDGSLYTC 120  
DB 61 EWFYREGGKDFLIYERYNGHGVESPPQGRLOMNGSKDLQDVSTIVLVNTLNDGSLYTC 120  
QY 121 NVSREFEFEHAPFVVTTLIPLRVTEAGDEFTSVSSIMTYILLVFLTLMIEMTYC 180  
DB 121 NVSREFEFEHAPFVVTTLIPLRVTEAGDEFTSVSSIMTYILLVFLTLMIEMTYC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
RESULT 9  
AAM79212  
ID AAM79212 standard; protein; 195 AA.

XX AAM79212;  
AC  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human protein SEQ ID NO 1874.  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN WO200157190-A2.  
XX  
XX  
PD 09-AUG-2001.  
XX  
PF 05-FEB-2001; 2001WO-US004098.  
XX  
XX 03-FEB-2000; 2000US-00496914.  
PR 27-APR-2000; 2000US-00560875.  
PR 20-JUN-2000; 2000US-00598075.  
PR 19-JUL-2000; 2000US-00620325.  
PR 01-SEP-2000; 2000US-00649361.  
PR 15-SEP-2000; 2000US-00663561.  
PR 20-OCT-2000; 2000US-00693325.  
PR 30-NOV-2000; 2000US-00728422.  
XX  
XX (HSE-) HSEQ INC.  
XX  
PA  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX  
DR WPI: 2001-476283/51.  
XX N-PSDB; AAK52345.  
XX  
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful  
PT in diagnosis and gene therapy.  
XX  
PS Claim 20; Page 4260; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC treatment/inhibitin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the  
CC sequence listing were missing at the time of publication  
XX  
SQ Sequence 195 AA;  
Query Match 89.7%; Score 1009; DB 4; Length 195;  
Best Local Similarity 98.5%; Pred. No. 2e-88;  
Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 121 NVSRFEFPAHRPFVKTTRLPLRVTEAGEDFTSVSEIMYILLVFLTLMLFTMIYC 180  
QY 181 YRKVSKAEAAQENA 195  
DB 181 YRKVSKAEAAQENA 195  
RESULT 10  
AAB50245  
ID AAB50245 standard; protein; 191 AA.  
XX  
AC AAB50245;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Rat sodium channel beta3 protein A1rx94h5 mature protein.  
XX  
KW Rat; sodium channel beta3 protein; A1rx94h5; pain; sleep disorder;  
KW neurodegenerative disorder; mood disorder; muscle contraction.  
XX  
OS Rattus sp.  
XX  
PN WO200069912-A1.  
XX  
PD 23-NOV-2000.  
XX  
PF 12-MAY-2000; 2000WO-US013144.  
XX  
PR 14-MAY-1999; 99US-0134198P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Curtis RAJ;  
XX  
DR WPI: 2001-122743/13.  
XX N-PSDB; AAC90600.  
XX  
PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal  
PT root ganglion cDNA library for use in chromosome mapping, forensic  
PT medicine, monitoring clinical trials and therapeutics.  
XX  
PS Claim 9; Fig 2; 145pp; English.  
XX  
XX The present invention provides the protein and coding sequences of the  
CC rat sodium channel beta3 protein, designated A1rx94h5. This protein is  
CC involved in the generation of pain and other sensory or perceptive nerve  
CC impulses, in the establishment and endurance of mood, neurodegenerative  
CC and sleep disorders, and in the control of muscle contraction, including  
CC movements such as the heartbeat, digestion and vascular tone. The  
CC sequences can be used in predictive medicine, screening and diagnostic  
CC assays, and in pharmacogenomics  
XX  
SQ Sequence 191 AA;  
Query Match 88.5%; Score 996; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 3.4e-87;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 11

ABG22577 standard; protein; 369 AA.

AC ABG22577;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22568.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

PI MPI; 2001-639362/73.

DR N-PSDB; AAS6764.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensic, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

PS Claim 20; SEQ ID NO 52936; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polynucleotide and polynucleotide sequences have applications in diagnostics, forensic, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 369 AA;

Query Match 82.4%; Score 927.5; DB 4; Length 369;

Best Local Similarity 92.3%; Pred. No. 2.8e-80;

Matches 181; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY 1 MPANFLPLASLVLYWVRCVPCVSETEAVQGNPMKLRICISCKRREVEATTYV 59  
DB 127 MPANFLPLASLVLYWVRCVPCVSETEAVQGNPMKLRICISCKRREVEATTYV 186  
QY 60 VEMFYRPEGKDLIYEVNRNGHQBVSPPQGRLOMNGSKDLOVSTIVNLINDSGLYT 119

DB 187 VEMFYRPEGKDLIYEVNRNGHQBVSPPQGRLOMNGSKDLOVSTIVNLINDSGLYT 246

QY 120 CNVSREFPEBAHPPFKITRLIPLRTEBAGBDFTSVSEIMMYILLVLTMLFLEMITY 179

DB 247 CNVSREFPEBAHPPFKITRLIPLRTEBAGBDFTSVSEIMMYILLVLTMLFLEMITY 306

QY 180 CYRKVSKAEBAQENA 195

DB 307 CYRKVSKAEBAQENA 322

## RESULT 12

AAB36021 standard; protein; 159 AA.

AC AAB36021;

DT 15-FEB-2001 (first entry)

DE Rat beta3 subunit peptide, SEQ ID NO: 23.

KW Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;

KW vasotrophic; cardiant; nocotrophic; cytostatic; dermatological;

KW gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;

KW ischaemia; heart disease; Jacobsen Syndrome; familial nonchromaffin paraganglioma; phenylketonuria;

KW Charcot Marie Tooth disease.

OS Rattus sp.

PN WO200063367-A1.

PD 26-OCT-2000.

PF 24-FEB-2000; 2000WO-EP001783.

PR 15-APR-1999; 99US-0129473P.

PA (WARN) WARNER LAMBERT CO.

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI Cox P, Dixon A, Jackson A, Morgan K;

PI MPI; 2000-665241/64.

PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke.

PS Claim 36; Page 76-77; 88pp; English.

The present sequence is given in the claims of a specification relating to a novel family of beta sub-unit proteins from a voltage-gated sodium channel. Human and rat beta sub-units, which have been collectively identified as beta3, have been isolated. The polynucleotides and polypeptides are useful for screening for agonists and antagonists of sodium channels. The agonists, antagonists, proteins and nucleic acids may be used diagnosing of treating diseases or conditions associated with voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia, heart disease, Jacobsen Syndrome, familial Nonchromaffin Paraganglioma, phenylketonuria and Charcot Marie Tooth disease

SQ Sequence 159 AA;

Query Match 74.8%; Score 842; DB 3; Length 159;

Best Local Similarity 100.0%; Pred. No. 1.6e-72;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANFLPLASLVLYWVRCVPCVSETEAVQGNPMKLRICISCKRREVEATTYV 60  
DB 1 MPANFLPLASLVLYWVRCVPCVSETEAVQGNPMKLRICISCKRREVEATTYV 60

QY 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLDVSIITVNTVLTNDLSGLYTC 120  
DB 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLDVSIITVNTVLTNDLSGLYTC 120  
QY 121 NVSRFEFEARHPFYKTRLLIPLRVTBEAGDEFTSVSE 159  
DB 121 NVSRFEFEARHPFYKTRLLIPLRVTBEAGDEFTSVSE 159

## RESULT 13

AAB36020  
ID AAB36020 standard; protein; 159 AA.

AC AAB36020;  
XX  
XX 15-FEB-2001 (first entry)  
DT  
DE Human beta3 subunit peptide, SEQ ID NO: 22.

XX Human; beta sub-unit; beta3; analgesic; anticonvulsant;  
XX cerebroprotective; vasotropic; cardiac; nootropic; cytostatic;  
XX dermatological; gene therapy; voltage-gated sodium channel; pain;  
XX epilepsy; stroke; ischaemia; heart disease; Jacobson Syndrome;  
XX familial nonchromaffin paraganglioma; phenylketonuria;  
XX Charcot Marie Tooth disease.

XX Homo sapiens.

XX WO200063367-A1.

XX 26-OCT-2000.

XX 24-FEB-2000; 2000WO-EP001783.

XX 15-APR-1999; 99US-0129473P.

XX (WARN ) WARNER LAMBERT CO.  
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;  
XX WPI; 2000-665241/64.

XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium  
XX channel, and their corresponding polypeptides, useful for detecting and  
XX treating sodium channel-associated conditions, e.g. pain, epilepsy and  
XX stroke.

XX Claim 36; Page 76; 88pp; English.

XX The present sequence is given in the claims of a specification relating  
XX to a novel family of beta sub-unit proteins from a voltage-gated sodium  
XX channel. Human and rat beta sub-units, which have been collectively  
XX identified as beta3, have been isolated. The polynucleotides and  
XX polypeptides are useful for screening for agonists and antagonists of  
XX sodium channels. The agonists, antagonists, proteins and nucleic acids  
XX may be used for diagnosing of treating diseases or conditions associated with  
XX voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,  
XX heart disease, Jacobson Syndrome, Familial Nonchromaffin Paraganglioma,  
XX Phenylketonuria and Charcot Marie Tooth disease

XX Sequence 159 AA;

Query Match 74.0%; Score 832; DB 3; Length 159;  
Best Local Similarity 98.7%; Pred. No. 1.4e-71;  
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVIYWRVCPVCVPSSTEAIVQGNPKLRICISCKRBEVATTIV 60  
DB 1 MPAFRLPLASLVIYWRVCPVCVPSSTEAIVQGNPKLRICISCKRBEVATTIV 60  
QY 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLDVSIITVNTVLTNDLSGLYTC 120

DB 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLDVSIITVNTVLTNDLSGLYTC 120  
QY 121 NVSRFEFEARHPFYKTRLLIPLRVTBEAGDEFTSVSE 159  
DB 121 NVSRFEFEARHPFYKTRLLIPLRVTBEAGDEFTSVSE 159

## RESULT 14

ADSI0835  
ID ADSI0835 standard; protein; 157 AA.

AC ADSI0835;  
XX  
XX 16-DEC-2004 (first entry)  
DT

XX Human therapeutic protein - SEQ ID 1072.  
DE

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;  
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
XX aplastic anaemia; cancer; wound healing; gene therapy.

XX Homo sapiens.

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YF, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX WPI; 2004-668857/65.

XX DR N-PSDB; ADSI0151.

XX New polynucleotide, useful in preparing a composition for diagnosing or  
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
XX aplastic anemia or cancer for promoting wound healing.

XX Claim 20; SEQ ID NO 1072; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded  
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,  
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may  
XX be useful in preparing a composition for diagnosing or treating  
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
XX disorders, such as aplastic anaemia or cancer, as well as for promoting  
XX wound healing. The molecules may also be utilised during gene therapy  
XX procedures. The current sequence is that of a human therapeutic protein  
XX of the invention. The current sequence is not shown explicitly within the  
XX specification but can be accessed from the WIPO web-site.

XX Sequence 157 AA;

Query Match 73.2%; Score 823; DB 8; Length 157;  
Best Local Similarity 98.7%; Pred. No. 1e-70;  
Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVIYWRVCPVCVPSSTEAIVQGNPKLRICISCKRBEVATTIV 60  
DB 1 MPAFRLPLASLVIYWRVCPVCVPSSTEAIVQGNPKLRICISCKRBEVATTIV 60  
QY 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLDVSIITVNTVLTNDLSGLYTC 120  
DB 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLDVSIITVNTVLTNDLSGLYTC 120  
QY 121 NVSRFEFEARHPFYKTRLLIPLRVTBEAGDEFTSVV 157

Db 121 NVSREFFFEAHRPFVKTRLLPLRVTEAGEDFTSV 157

## RESULT 15

ID ABG22576 standard; protein; 1176 AA.

AC ABG22576;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22567.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX

**XX**

XX  
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9  
9  
9  
9  
9  
9

2 XX

**XXXXXXXXXXXX**

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

Drmanac RT, Liu C

DR WPI; 2001-639362/73.

XX

PT diagnostics, forensic

PT biodiversity.

PS Claim 20; SEQ ID NO 52935; 103bp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [http://wipo.int/pub/published/pct\\_sequences](http://wipo.int/pub/published/pct_sequences)

**SQ Sequence 1176 AA;**

Query Match	Score	DB	Length
61.2%	689	4	1176

```
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 19 VRVFPCVCEVPSETEAVOGNPMKLRCSOMKREVEATVVWVYRPEGGKDFLIYEYR 78

Db 987 VSVCFPVCEVPSSETEAVOGNPMKLRCSOMKREVEATVVWVYRPEGGKDFLIYEYR 1046

Db 987 VSVCFPVCVEVPSETEAVQGNPKLRICISCMKREVEATTVVEMFYRPEGKDFLYEYR 1046

79 NGHQEVESPFQGRLOWNGSKDLODV SITVLNVTLLND SGLYTCNVSRREEFEFEAH RPFVKTT 138

Db 1047 NGHQEVESPFQGR LQWNGSKDLQDV SITVLNT LND SGLYTCNVSREFEF EFAHRPFVKTT 1106

QY	139	RLPLRVTEE	148

D6 1107 RLIPLRVTEE 1116

```
Search completed: March 31, 2005, 20:17:51
Job time : 128.5 secs
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Job time : 128.5 secs

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GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 6658  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6658

Query Match 13.1%; Score 147.5; DB 4; Length 215;  
Best Local Similarity 27.9%; Pred. No. 8,5e-08;  
Matches 55; Conservative 27; Mismatches 72; Indels 43; Gaps 8;

QY 7 LPLASLVLIYVWVCFVPCVEPSETEAVQGNPKMKRCISCMKREBEVATTVEMFYRP 66  
DB 21 LMPILAA-VEIYTSRV-----LEAVNGTDARLKTFSFPAPVGDALVTI-WNFRP 67  
QY 67 -EGG-KDFLIYEYRNGHOEVESPPQGRLOWNSKDLQDVSTIVLNTLNSGLYTCVNSR 124  
DB 68 LDGGEQGFVYHYHIDPFQPMGSRFKDRVSWDGNPERDASILLMKLQDFDDNGTYTCQVKN 127  
QY 125 EEFPEAHRPVTTRLLPLRVTEAGEDFTSVV-----SEIMYLLV-----FLTLM 173  
DB 128 -----PPDVGVIGELIRLSVHTVRSEIHFLALAIQSACALMIITVI 170  
QY 174 FIEMTYCRKYSKAEAA 190  
DB 171 VVVLFGHYRKKRWAEAA 187

RESULT 3  
US-09-949-016-10819  
; Sequence 10819, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 10819  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10819

Query Match 13.1%; Score 147.5; DB 4; Length 263;  
Best Local Similarity 27.9%; Pred. No. 1.1e-07;  
Matches 55; Conservative 27; Mismatches 72; Indels 43; Gaps 8;

QY 7 LPLASLVLIYVWVCFVPCVEPSETEAVQGNPKMKRCISCMKREBEVATTVEMFYRP 66  
DB 7 LPLASLVLIYVWVCFVPCVEPSETEAVQGNPKMKRCISCMKREBEVATTVEMFYRP 66

DB 69 LMPILAA-VEIYTSRV-----LEAVNGTDARLKTFSFPAPVGDALVTI-WNFRP 115  
QY 67 -EGG-KDFLIYEYRNGHOEVESPPQGRLOWNSKDLQDVSTIVLNTLNSGLYTCVNSR 124  
DB 116 LDGGEQGFVYHYHIDPFQPMGSRFKDRVSWDGNPERDASILLMKLQDFDDNGTYTCQVKN 175  
QY 125 EEFPEAHRPVTTRLLPLRVTEAGEDFTSVV-----SEIMYLLV-----FLTLM 173  
DB 176 -----PPDVGVIGELIRLSVHTVRSEIHFLALAIQSACALMIITVI 218  
QY 174 FIEMTYCRKYSKAEAA 190  
DB 219 VVVLFGHYRKKRWAEAA 235

RESULT 4  
US-09-430-503-2  
; Sequence 2, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME  
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-2

Query Match 11.6%; Score 131; DB 3; Length 269;  
Best Local Similarity 23.0%; Pred. No. 7.1e-06;  
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPESETEAVQGNPKMKRCISCMKREBEVATTVEMFYRPFGKDFL-IYERYNGHQ 82  
DB 40 VYTPKEIRIVANGTQKLTIC-----KFKSTTGGTISVNSFPQEGADTVTFPHYSQGV 95  
QY 83 EVES--PPQGRLOWNSKDLQDVSTIVLNTLNSGLYTCVNSREFEAHRPVTTRRL 140  
DB 96 YLGNYPPFKDRISVAGDIDKDKDASINIMQGFHNGTYICVKN----- 139  
QY 141 IPLRVTEAGEDFTSVSE-----IMMYLLVFLTLMFIEMTYC--YRK----- 183  
DB 140 -PPDIVQPGHRIYVVEKENLPVFPVWVVGIVAVVLGLTLLISMLAVLYRKKNSKR 198  
QY 184 -----VSKAEAAQENASD-----YLAIPSENKENVV 211  
DB 199 DYTGCSTSESISPVKQAPRKSPSTEGLYKSLPSGSHQGPVI 240

RESULT 5  
US-09-430-503-4  
; Sequence 4, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME  
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-4



Query Match 11.6%; Score 131; DB 3; Length 269;  
 Best Local Similarity 23.0%; Pred. No. 7.1e-06;  
 Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSSEAVQGNPKLRICISCKRREVEAT--TVWVFYRPGGKDFL-IEYRNGHQ 82  
 DB 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGLTSVMSFQEGADTVTSFPHYSGQV 95  
 QY 83 EVES--PFGRLQWNSKDLQDVSTIVLNTLNDGSLYTGNVSRREFEFAHRPFVKTTRL 140  
 DB 96 YLGNYPFPKDRISMAGDLDDKDKASINENMQFIHNGTYICDVKN-----139  
 QY 141 IPLRVTEAGEDTSTVSE-----IMMYILVFLTLMLFIEMTYC--YRK-----183  
 DB 140 -PDIIVQPGHIRLHYVEKENLVPFVWVVGIVTAVLGLTLISMLAVLYRRKNSKR 198  
 QY 184 -----VSKAEBAQENASD---YLAIPSENKENS V 211  
 DB 199 DYTGCSTSESLSPVKAQPRKSPSDTEGLVKSLSGSHQGPVI 240

RESULT 6  
 US-09-430-503-6  
 ; Sequence 6, Application US/09430503  
 ; Patent No. 6355786  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhao, Zhizhuang  
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
 ; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME  
 ; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2  
 ; CURRENT FILING DATE: 1999-10-29  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 269  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-430-503-6

Query Match 11.6%; Score 131; DB 3; Length 269;  
 Best Local Similarity 23.0%; Pred. No. 7.1e-06;  
 Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSSEAVQGNPKLRICISCKRREVEAT--TVWVFYRPGGKDFL-IEYRNGHQ 82  
 DB 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGLTSVMSFQEGADTVTSFPHYSGQV 95  
 QY 83 EVES--PFGRLQWNSKDLQDVSTIVLNTLNDGSLYTGNVSRREFEFAHRPFVKTTRL 140  
 DB 96 YLGNYPFPKDRISMAGDLDDKDKASINENMQFIHNGTYICDVKN-----139  
 QY 141 IPLRVTEAGEDTSTVSE-----IMMYILVFLTLMLFIEMTYC--YRK-----183  
 DB 140 -PDIIVQPGHIRLHYVEKENLVPFVWVVGIVTAVLGLTLISMLAVLYRRKNSKR 198  
 QY 184 -----VSKAEBAQENASD---YLAIPSENKENS V 211  
 DB 199 DYTGCSTSESLSPVKAQPRKSPSDTEGLVKSLSGSHQGPVI 240

RESULT 7  
 US-09-430-503-8  
 ; Sequence 8, Application US/09430503  
 ; Patent No. 6355786  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhao, Zhizhuang  
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
 ; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME  
 ; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2  
 ; CURRENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 269  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-430-503-8

Query Match 11.6%; Score 131; DB 3; Length 269;  
 Best Local Similarity 23.0%; Pred. No. 7.1e-06;  
 Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSSEAVQGNPKLRICISCKRREVEAT--TVWVFYRPGGKDFL-IEYRNGHQ 82  
 DB 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGLTSVMSFQEGADTVTSFPHYSGQV 95  
 QY 83 EVES--PFGRLQWNSKDLQDVSTIVLNTLNDGSLYTGNVSRREFEFAHRPFVKTTRL 140  
 DB 96 YLGNYPFPKDRISMAGDLDDKDKASINENMQFIHNGTYICDVKN-----139  
 QY 141 IPLRVTEAGEDTSTVSE-----IMMYILVFLTLMLFIEMTYC--YRK-----183  
 DB 140 -PDIIVQPGHIRLHYVEKENLVPFVWVVGIVTAVLGLTLISMLAVLYRRKNSKR 198  
 QY 184 -----VSKAEBAQENASD---YLAIPSENKENS V 211  
 DB 199 DYTGCSTSESLSPVKAQPRKSPSDTEGLVKSLSGSHQGPVI 240

RESULT 8  
 US-09-949-016-10974  
 ; Sequence 10974, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241, 755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237, 768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231, 498  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10974  
 ; LENGTH: 313  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-949-016-10974

Query Match 11.6%; Score 131; DB 4; Length 313;  
 Best Local Similarity 23.0%; Pred. No. 8.8e-06;  
 Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSSEAVQGNPKLRICISCKRREVEAT--TVWVFYRPGGKDFL-IEYRNGHQ 82  
 DB 84 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGLTSVMSFQEGADTVTSFPHYSGQV 139  
 QY 83 EVES--PFGRLQWNSKDLQDVSTIVLNTLNDGSLYTGNVSRREFEFAHRPFVKTTRL 140  
 DB 140 YLGNYPFPKDRISMAGDLDDKDKASINENMQFIHNGTYICDVKN-----183  
 QY 141 IPLRVTEAGEDTSTVSE-----IMMYILVFLTLMLFIEMTYC--YRK-----183  
 DB 184 -PDIIVQPGHIRLHYVEKENLVPFVWVVGIVTAVLGLTLISMLAVLYRRKNSKR 242  
 QY 184 -----VSKAEBAQENASD---YLAIPSENKENS V 211  
 DB 243 DYTGCSTSESLSPVKAQPRKSPSDTEGLVKSLSGSHQGPVI 284

## RESULT 9

US-09-430-503-26

; Sequence 26, Application US/09430503

; Patent No. 6355786

; GENERAL INFORMATION:

; APPLICANT: Zhao, Zhizhuang

; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND

; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2

; CURRENT APPLICATION NUMBER: US/09/430,503

; CURRENT FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 26

; LENGTH: 270

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-430-503-26

Query Match 11.2%; Score 126.5; DB 3; Length 270;

Best Local Similarity 26.9%; Pred. No. 2,2e-05;

Matches 54; Conservative 29; Mismatches 89; Indels 29; Gaps 10;

QY 2 PAFNRL--PLASLVLIYWRVCPVCEVPESTEAVOGNPMKLCISCMKREEVEAT-- 57

DB 14 PARRRWLSVLAAMGLTARIS-ALVHTPKRIIVVNGTQKLTCTF----DSPNTTGW 68

QY 58 -TVWEMFYRPEGKDFL-IYEYRNGHOVES--PQGRLOWNGSKDLDVSTIVLVNTLN 113

DB 69 LTTVWSMSPQDGTDSAVSFFHYSQGVYIGDYPPEKDRVTAGDLDKDKDASININIQAV 128

QY 114 DSGLYTCVNSREFEFAHRP-----FKTTRLILPRTVEAGDFTSVSEIMMYILLV 167

DB 129 HNGTYICVKNPDDIV-RPGHRLHVAIDNLVFLVWVVVG-TVTAVVGLTLLISLV 186

QY 168 FLTLMFLFEMICYRKVSKE 188

DB 187 LVLYL-----RKHSKRD 199

## RESULT 10

US-09-430-503-30

; Sequence 30, Application US/09430503

; Patent No. 6355786

; GENERAL INFORMATION:

; APPLICANT: Zhao, Zhizhuang

; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND

; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2

; CURRENT APPLICATION NUMBER: US/09/430,503

; CURRENT FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 30

; LENGTH: 270

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-430-503-30

Query Match 11.2%; Score 126.5; DB 3; Length 270;

Best Local Similarity 26.9%; Pred. No. 2,2e-05;

Matches 54; Conservative 29; Mismatches 89; Indels 29; Gaps 10;

QY 2 PAFNRL--PLASLVLIYWRVCPVCEVPESTEAVOGNPMKLCISCMKREEVEAT-- 57

DB 14 PARRRWLSVLAAMGLTARIS-ALVHTPKRIIVVNGTQKLTCTF----DSPNTTGW 68

QY 58 -TVWEMFYRPEGKDFL-IYEYRNGHOVES--PQGRLOWNGSKDLDVSTIVLVNTLN 113

DB 69 LTTVWSMSPQDGTDSAVSFFHYSQGVYIGDYPPEKDRVTAGDLDKDKDASININIQAV 128

QY 114 DSGLYTCVNSREFEFAHRP-----FKTTRLILPRTVEAGDFTSVSEIMMYILLV 167

DB 129 HNGTYICVKNPDDIV-RPGHRLHVAIDNLVFLVWVVVG-TVTAVVGLTLLISLV 186

QY 168 FLTLMFLFEMICYRKVSKE 188

DB 187 LVLYL-----RKHSKRD 199

## RESULT 11

US-09-430-503-44

; Sequence 44, Application US/09430503

; Patent No. 6355786

; GENERAL INFORMATION:

; APPLICANT: Zhao, Zhizhuang

; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND

; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2

; CURRENT APPLICATION NUMBER: US/09/430,503

; CURRENT FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 44

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-430-503-44

Query Match 11.1%; Score 125; DB 3; Length 199;

Best Local Similarity 25.4%; Pred. No. 2e-05;

Matches 46; Conservative 21; Mismatches 74; Indels 40; Gaps 7;

QY 27 VEVPSETEAVOGNPMKLCISCMKREEVEAT--TVWEMFYRPEGKDFL-IYEYRNGHQ 82

DB 40 VYTPKEIRIVVANGTQKLTCTF-----KFKSTTGTGLTSVMSFGADTTSVFFHYSQGV 95

QY 83 EVES--PQGRLOWNGSKDLDVSTIVLVNTLNDGLTYCVNSREFEFAHRPFVKTTRL 140

DB 96 YIGNYPPEKDRISWAGDLDKDKDASININEMQFIHNGTYICVKN----- 139

QY 141 IPLRTEAGDFTSVSE-----IMMYILLVFLTLMFLFEMICYC--RKVSKE 187

DB 140 -PPDIVPQGHIRLYYVEKENLPVFPVWVVVGIVAVVGLTLLISLMLAVYRKSKSR 198

QY 188 E 188

DB 199 D 199

## RESULT 12

US-09-430-503-48

; Sequence 48, Application US/09430503

; Patent No. 6355786

; GENERAL INFORMATION:

; APPLICANT: Zhao, Zhizhuang

; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND

; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2

; CURRENT APPLICATION NUMBER: US/09/430,503

; CURRENT FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 48

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-430-503-48

Query Match 11.1%; Score 125; DB 3; Length 199;

Best Local Similarity 25.4%; Pred. No. 2e-05;

Matches 46; Conservative 21; Mismatches 74; Indels 40; Gaps 7;

QY 27 VEVPSETEAVOGNPMKLCISCMKREEVEAT--TVWEMFYRPEGKDFL-IYEYRNGHQ 82

Db 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGGTISVSWGFEQEGADTTVSFPHYSOGQV 95  
QY 83 EVES--PFGRLQWNGSKDLOVSIYLVNLTNDGSLYTCNVSREPEFAHRPFVKTTRL 140  
Db 96 YIGNYPFDKRIISWAGDLDKQDASINIEHQFIHNGTYICDVKN-----139  
QY 141 IPLRTEAGEDFTSVSE-----IMMYILLVFLTLMFIEMICY--RKVSKA 187  
Db 140 -PEDIYVQGHRIYVEKENLVPFVWVVGIVTAVVLGTLTLLISMLAVLYRRKNSKR 198  
QY 188 E 188  
Db 199 D 199

RESULT 13  
US-09-430-503-28  
; Sequence 28, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-430-503-28

Query Match 11.1%; Score 125; DB 3; Length 270;  
Best Local Similarity 27.0%; Pred. No. 3.2e-05;  
Matches 47; Conservative 23; Mismatches 78; Indels 26; Gaps 8;

QY 27 VEVPSTEAQGNPMKLRICISCKREVEAT--TYVEMFYRPEGKDFL-IYERNHQ 82  
Db 40 VHTPKEIFVANGTQGLTCTF---DSPNTGMLTIVSWSFQPDGDSAVSFPHYSOGQV 95  
QY 83 EVES--PFGRLQWNGSKDLOVSIYLVNLTNDGSLYTCNVSREPEFAHRPFVKTTRL 134  
Db 96 YIGDYPPFDKRIISWAGDLDKQDASINIEHQFIHNGTYICDVKNPPDIYV-RGHIRLHV 154  
QY 135 VKTTRLIPLRTEAGEDFTSVSEIMMYILLVFLTLMFIEMICYRKVSKAE 188  
Db 155 VEIDNLVFLVWVVG-TVTAVVLGTLTLLISLVLVLY-----RRKSKRD 199

RESULT 14  
US-09-430-503-32  
; Sequence 32, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-430-503-32

Query Match 11.1%; Score 125; DB 3; Length 270;  
Best Local Similarity 27.0%; Pred. No. 3.2e-05;

Matches 47; Conservative 23; Mismatches 78; Indels 26; Gaps 8;  
QY 27 VEVPSTEAQGNPMKLRICISCKREVEAT--TYVEMFYRPEGKDFL-IYERNHQ 82  
Db 40 VHTPKEIFVANGTQGLTCTF---DSPNTGMLTIVSWSFQPDGDSAVSFPHYSOGQV 95  
QY 83 EVES--PFGRLQWNGSKDLOVSIYLVNLTNDGSLYTCNVSREPEFAHRPFVKTTRL 134  
Db 96 YIGDYPPFDKRIISWAGDLDKQDASINIEHQFIHNGTYICDVKNPPDIYV-RGHIRLHV 154  
QY 135 VKTTRLIPLRTEAGEDFTSVSEIMMYILLVFLTLMFIEMICYRKVSKAE 188  
Db 155 VEIDNLVFLVWVVG-TVTAVVLGTLTLLISLVLVLY-----RRKSKRD 199

RESULT 15  
US-09-430-503-42  
; Sequence 42, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-42

Query Match 10.9%; Score 123; DB 3; Length 199;  
Best Local Similarity 25.4%; Pred. No. 3.4e-05;  
Matches 46; Conservative 21; Mismatches 74; Indels 40; Gaps 7;

QY 27 VEVPSTEAQGNPMKLRICISCKREVEAT--TYVEMFYRPEGKDFL-IYERNHQ 82  
Db 40 VHTPKEIFVANGTQGLTCTC---KFKSTSTTGGTISVSWGFEQEGADTTVSFPHYSOGQV 95  
QY 83 EVES--PFGRLQWNGSKDLOVSIYLVNLTNDGSLYTCNVSREPEFAHRPFVKTTRL 140  
Db 96 YIGNYPFDKRIISWAGDLDKQDASINIEHQFIHNGTYICDVKN-----139  
QY 141 IPLRTEAGEDFTSVSE-----IMMYILLVFLTLMFIEMICY--RKVSKA 187  
Db 140 -PEDIYVQGHRIYVEKENLVPFVWVVGIVTAVVLGTLTLLISMLAVLYRRKNSKR 198  
QY 188 E 188  
Db 199 D 199

Search completed: March 31, 2005, 20:23:54  
Job time : 32 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: March 31, 2005, 20:21:59 ; Search time 91.5 Seconds  
(without alignments)  
779.153 Million cell updates/sec

Title: US-09-977-579-1

Perfect score: 1125  
Sequence: 1 MPAFNRLLPLASLVLYWVR.....SDYLAIPISENKSNVYVBE 215

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
19: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1125	100.0	215	11	US-09-977-579-1
2	1125	100.0	215	13	US-10-029-191-2
3	1125	100.0	215	14	US-10-142-201B-12
4	1105	98.2	215	11	US-09-977-579-2
5	1105	98.2	215	14	US-10-142-201B-11
6	996	88.5	191	13	US-10-029-191-4
7	842	74.8	159	11	US-09-977-579-23
8	832	74.0	159	11	US-09-977-579-22
9	597	53.1	111	13	US-10-029-191-5
10	470.5	41.8	218	13	US-10-029-191-20
11	466.5	41.5	218	14	US-10-142-201B-8
12	466.5	41.5	218	16	US-10-477-272-2
13	463.5	41.2	218	11	US-09-977-579-44

14	292	26.0	58	13	US-10-029-191-7	Sequence 7, Appl
15	257.5	22.9	268	9	US-09-875-456A-14	Sequence 14, Appl
16	257.5	22.9	268	15	US-10-401-916-14	Sequence 14, Appl
17	230	20.4	74	15	US-10-276-774-2068	Sequence 2068, Ap
18	206	18.3	39	11	US-09-977-579-18	Sequence 18, Appl
19	196	17.4	39	11	US-09-977-579-17	Sequence 17, Appl
20	165	14.7	34	11	US-09-977-579-47	Sequence 47, Appl
21	164	14.6	248	15	US-10-016-248-54	Sequence 54, Appl
22	164	14.6	251	15	US-10-016-248-52	Sequence 52, Appl
23	164	14.6	258	15	US-10-016-248-53	Sequence 53, Appl
24	162	14.4	219	15	US-10-016-248-51	Sequence 51, Appl
25	161	14.3	34	11	US-09-977-579-31	Sequence 31, Appl
26	160	14.2	248	15	US-10-205-331-110	Sequence 110, Appl
27	153	13.6	248	14	US-10-272-601-1	Sequence 12, Appl
28	152	13.5	235	13	US-10-053-107-12	Sequence 12, Appl
29	152	13.5	235	14	US-10-227-884-238	Sequence 238, App
30	152	13.5	235	14	US-10-230-163-238	Sequence 238, App
31	152	13.5	235	14	US-10-230-338-238	Sequence 238, App
32	152	13.5	235	14	US-10-218-631-238	Sequence 238, App
33	152	13.5	235	14	US-10-230-414-238	Sequence 238, App
34	152	13.5	235	14	US-10-213-145-12	Sequence 12, Appl
35	152	13.5	235	14	US-10-232-228-238	Sequence 238, App
36	152	13.5	235	14	US-10-216-159A-238	Sequence 238, App
37	152	13.5	235	14	US-10-218-849-238	Sequence 238, App
38	152	13.5	235	14	US-10-227-873-238	Sequence 238, App
39	152	13.5	235	14	US-10-227-883-238	Sequence 238, App
40	152	13.5	235	14	US-10-219-076-238	Sequence 238, App
41	152	13.5	235	14	US-10-230-434-238	Sequence 238, App
42	152	13.5	235	14	US-10-213-199-12	Sequence 12, Appl
43	152	13.5	235	14	US-10-219-003-238	Sequence 238, App
44	152	13.5	235	14	US-10-219-075-238	Sequence 238, App
45	152	13.5	235	14	US-10-219-464-238	Sequence 238, App

#### ALIGNMENTS

RESULT 1  
US-09-977-579-1  
; Sequence 1, Application US/09977579  
; Publication No. US20040248240A1  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge University Technical Services  
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi  
; TITLE OF INVENTION: channel  
; FILE REFERENCE: 674558-2001  
; CURRENT APPLICATION NUMBER: US/09/977, 579  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP00/01783  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60,129,473  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 1  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-977-579-1

Query Match 100.0%; Score 1125; DB 11; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.8e-105; Indels 0; Gaps 0;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPAFNRLLPLASLVLYWVRCPVCEVPSSEAVQGNPMKURCTSCMKRBEVEATTVV 60  
DB 1 MPAFNRLLPLASLVLYWVRCPVCEVPSSEAVQGNPMKURCTSCMKRBEVEATTVV 60  
QY 61 EMFYREGGKDFIYYRRNGHGVESPFGRLQWNSKLDVSTIVLVNTLNDGLYTC 120  
DB 61 EMFYREGGKDFIYYRRNGHGVESPFGRLQWNSKLDVSTIVLVNTLNDGLYTC 120

Qy 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMLFIEMTYC 180  
Db 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMLFIEMTYC 180  
Qy 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215  
Db 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

## RESULT 2

US-10-029-191-2  
; Sequence 2, Application US/10029191  
; Publication No. US20020160453A1  
; GENERAL INFORMATION:  
; APPLICANT: CURTIS, ROY A.J.  
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
; TITLE OF INVENTION: PROTEIN  
; FILE REFERENCE: 210147.00X/5U1  
; CURRENT APPLICATION NUMBER: US/10/029,191  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/569,978  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/134,198  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-029-191-2

Query Match 100.0%; Score 1125; DB 13; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.8e-105;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAFRLPLASLVLIYWRVCFVCEVPSSETAVQGNPKLRCISCMKREBEVATTIV 60  
Db 1 MPAFRLPLASLVLIYWRVCFVCEVPSSETAVQGNPKLRCISCMKREBEVATTIV 60  
Qy 61 EMFYRPEGKDFLIYENRNGHOEVSPQGRLOMNGSKDLOVSTIVLVNTLNDGSLYTC 120  
Db 61 EMFYRPEGKDFLIYENRNGHOEVSPQGRLOMNGSKDLOVSTIVLVNTLNDGSLYTC 120  
Qy 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMLFIEMTYC 180  
Db 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMLFIEMTYC 180  
Qy 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215  
Db 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

## RESULT 3

US-10-142-201B-12  
; Sequence 12, Application US/10142201B  
; Publication No. US20030022205A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; APPLICANT: Curtis, Roy A.J.  
; TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MP2001-106PLRN(M)  
; CURRENT APPLICATION NUMBER: US/10/142,201B  
; CURRENT FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: US 60/289,893  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus

US-10-142-201B-12

Query Match 100.0%; Score 1125; DB 14; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.8e-105;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAFRLPLASLVLIYWRVCFVCEVPSSETAVQGNPKLRCISCMKREBEVATTIV 60  
Db 1 MPAFRLPLASLVLIYWRVCFVCEVPSSETAVQGNPKLRCISCMKREBEVATTIV 60  
Qy 61 EMFYRPEGKDFLIYENRNGHOEVSPQGRLOMNGSKDLOVSTIVLVNTLNDGSLYTC 120  
Db 61 EMFYRPEGKDFLIYENRNGHOEVSPQGRLOMNGSKDLOVSTIVLVNTLNDGSLYTC 120  
Qy 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMLFIEMTYC 180  
Db 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMLFIEMTYC 180  
Qy 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215  
Db 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

## RESULT 4

US-09-977-579-2  
; Sequence 2, Application US/09977579  
; Publication No. US20040248240A1  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge University Technical Services  
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi  
; TITLE OF INVENTION: channel  
; FILE REFERENCE: 674558-2001  
; CURRENT APPLICATION NUMBER: US/09/977,579  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP00/01783  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60,129,473  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-977-579-2

Query Match 98.2%; Score 1105; DB 11; Length 215;  
Best Local Similarity 98.1%; Pred. No. 3e-103;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPAFRLPLASLVLIYWRVCFVCEVPSSETAVQGNPKLRCISCMKREBEVATTIV 60  
Db 1 MPAFRLPLASLVLIYWRVCFVCEVPSSETAVQGNPKLRCISCMKREBEVATTIV 60  
Qy 61 EMFYRPEGKDFLIYENRNGHOEVSPQGRLOMNGSKDLOVSTIVLVNTLNDGSLYTC 120  
Db 61 EMFYRPEGKDFLIYENRNGHOEVSPQGRLOMNGSKDLOVSTIVLVNTLNDGSLYTC 120  
Qy 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMLFIEMTYC 180  
Db 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMLFIEMTYC 180  
Qy 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215  
Db 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

## RESULT 5

US-10-142-201B-11  
; Sequence 11, Application US/10142201B  
; Publication No. US20030022205A1  
; GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals Inc.  
APPLICANT: Curtis, Rory A.J.  
TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,  
TITLE OF INVENTION: AND USES THEREFOR  
FILE REFERENCE: MP12001-106PRN(M)  
CURRENT APPLICATION NUMBER: US/10/142, 201B  
CURRENT FILING DATE: 2002-05-09  
PRIOR APPLICATION NUMBER: US 60/289,893  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 215  
TYPE: PRN  
ORGANISM: Homo sapiens  
US-10-142-201B-11

Query Match 98.2%; Score 1105; DB 14; Length 215;  
Best Local Similarity 98.1%; Pred. No. 3e-103;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPANRLPLASVLIYWRVCPVCEVPSSETEAVOGNPMKLRCSCKREEVEATTVV 60  
DB 1 MPANRLPLASVLIYWRVCPVCEVPSSETEAVOGNPMKLRCSCKREEVEATTVV 60  
QY 61 EWFYRPGGKDFLIYVRNGHVESPFQGRLOMNSKDLQDVSIYLVNTLNDGSLYTC 120  
DB 61 EWFYRPGGKDFLIYVRNGHVESPFQGRLOMNSKDLQDVSIYLVNTLNDGSLYTC 120  
QY 121 NVSRFEFEFAHPPVKTTRILPLRVTEBAGEDFTSVSEIMMYILVFLTMLFIEMITC 180  
DB 121 NVSRFEFEFAHPPVKTTRILPLRVTEBAGEDFTSVSEIMMYILVFLTMLFIEMITC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVVEE 215

RESULT 6  
US-10-029-191-4  
Sequence 4, Application US/10029191  
Publication No. US20020160453A1  
GENERAL INFORMATION:  
APPLICANT: CURTIS, RORY A.J.  
TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
FILE REFERENCE: 210147.00XX/5U1  
CURRENT APPLICATION NUMBER: US/10/029, 191  
CURRENT FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 09/569, 978  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/134, 198  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 191  
TYPE: PRN  
ORGANISM: Rattus sp.  
US-10-029-191-4

Query Match 88.5%; Score 996; DB 13; Length 191;  
Best Local Similarity 100.0%; Pred. No. 2.6e-92;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 VCVEVSETEAVOGNPMKLRCSCKREEVEATTVVWFYRPGGKDFLIYVRNGHVEV 84  
DB 1 VCVEVSETEAVOGNPMKLRCSCKREEVEATTVVWFYRPGGKDFLIYVRNGHVEV 84  
QY 85 ESWPQGRLOMNSKDLQDVSIYLVNTLNDGSLYTCVNSRFEFEFAHPPVKTTRILPLR 144  
DB 61 ESWPQGRLOMNSKDLQDVSIYLVNTLNDGSLYTCVNSRFEFEFAHPPVKTTRILPLR 120

QY 145 VTEBAGEDFTSVSEIMMYILVFLTMLFIEMITCYRKVSKAEBAQENASDYLAIPSE 204  
DB 121 VTEBAGEDFTSVSEIMMYILVFLTMLFIEMITCYRKVSKAEBAQENASDYLAIPSE 180  
QY 205 NKENSAPVVEE 215  
DB 181 NKENSAPVVEE 191

RESULT 7  
US-09-977-579-23  
Sequence 23, Application US/09977579  
Publication No. US20040248240A1  
GENERAL INFORMATION:  
APPLICANT: Cambridge University Technical Services  
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi  
TITLE OF INVENTION: channel  
FILE REFERENCE: 674558-2001  
CURRENT APPLICATION NUMBER: US/09/977, 579  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: PCT/EP00/01783  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60,129,473  
PRIOR FILING DATE: 2000-02-24  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 23  
LENGTH: 159  
TYPE: PRN  
ORGANISM: Rat  
US-09-977-579-23

Query Match 74.8%; Score 842; DB 11; Length 159;  
Best Local Similarity 100.0%; Pred. No. 7.4e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANRLPLASVLIYWRVCPVCEVPSSETEAVOGNPMKLRCSCKREEVEATTVV 60  
DB 1 MPANRLPLASVLIYWRVCPVCEVPSSETEAVOGNPMKLRCSCKREEVEATTVV 60  
QY 61 EWFYRPGGKDFLIYVRNGHVESPFQGRLOMNSKDLQDVSIYLVNTLNDGSLYTC 120  
DB 61 EWFYRPGGKDFLIYVRNGHVESPFQGRLOMNSKDLQDVSIYLVNTLNDGSLYTC 120  
QY 121 NVSRFEFEFAHPPVKTTRILPLRVTEBAGEDFTSVSE 159  
DB 121 NVSRFEFEFAHPPVKTTRILPLRVTEBAGEDFTSVSE 159

RESULT 8  
US-09-977-579-22  
Sequence 22, Application US/09977579  
Publication No. US20040248240A1  
GENERAL INFORMATION:  
APPLICANT: Cambridge University Technical Services  
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi  
TITLE OF INVENTION: channel  
FILE REFERENCE: 674558-2001  
CURRENT APPLICATION NUMBER: US/09/977, 579  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: PCT/EP00/01783  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60,129,473  
PRIOR FILING DATE: 2000-02-24  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 159  
TYPE: PRN  
ORGANISM: Homo sapiens  
US-09-977-579-22

Query Match 74.0%; Score 832; DB 11; Length 159;  
Best Local Similarity 98.7%; Pred. No. 7.6e-76;  
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVIIYWRVCFVCEVPSSETEAVOGNPMKLRICSCMKREVEATTVV 60  
DB 1 MPAFRLPLASLVIIYWRVCFVCEVPSSETEAVOGNPMKLRICSCMKREVEATTVV 60  
QY 61 EHFYRPEGKDFLIYENRNGHOVESPGQRLQWNGSKDLOVSIITVNTLNDGLYTC 120  
DB 61 EHFYRPEGKDFLIYENRNGHOVESPGQRLQWNGSKDLOVSIITVNTLNDGLYTC 120  
QY 121 NVSRFEFEAHRPFVKTTRLLPLRVTAEAGDEFTSVSE 159  
DB 121 NVSRFEFEAHRPFVKTTRLLPLRVTAEAGDEFTSVSE 159

## RESULT 9

US-10-029-191-5  
; Sequence 5, Application US/10029191  
; Publication No. US20020160453A1  
; GENERAL INFORMATION:

; APPLICANT: CURTIS, ROY A.J.  
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
; FILE REFERENCE: 210147.00XX/501  
; CURRENT APPLICATION NUMBER: US/10/029,191  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/569,978  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/134,198  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-029-191-5

Query Match 53.1%; Score 597; DB 13; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2.6e-52;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 VCVEVPSSETEAVOGNPMKLRICSCMKREVEATTVVEMFPRGGKDFLIYENRNGHOV 84  
DB 1 VCVEVPSSETEAVOGNPMKLRICSCMKREVEATTVVEMFPRGGKDFLIYENRNGHOV 60  
QY 85 ESPFGRLQWNGSKDLOVSIITVNTLNDGLYTCNVSREFEFAHRPFV 135  
DB 61 ESPFGRLQWNGSKDLOVSIITVNTLNDGLYTCNVSREFEFAHRPFV 111

## RESULT 10

US-10-029-191-20  
; Sequence 20, Application US/10029191  
; Publication No. US20020160453A1  
; GENERAL INFORMATION:

; APPLICANT: CURTIS, ROY A.J.  
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
; FILE REFERENCE: 210147.00XX/501  
; CURRENT APPLICATION NUMBER: US/10/029,191  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/569,978  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/134,198  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patencin Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 218

; TYPE: PRT  
; ORGANISM: Lepus Sp.  
US-10-029-191-20

Query Match 41.8%; Score 470.5; DB 13; Length 218;  
Best Local Similarity 49.3%; Pred. No. 3.8e-39;  
Matches 105; Conservative 29; Mismatches 64; Indels 15; Gaps 6;

QY 6 RLPL-ASLVIIYWRVCFVCEVPSSETEAVOGNPMKLRICSCMKREVEATTVVEM 62  
DB 3 RLPLAVGAAALVSGAM-----GCVEVDSSETEAVOGNPMKLRICSCMKREVEATTVVEM 57  
QY 63 FYRPEGKDFLIYENRNGHOVESP--FGRLQWNGS--KDLOVSIITVNTLNDGL 116  
DB 58 TFRQGTBEFVKILRYENEVLQLEDERFEGRVVWNGSRGTKDLOLSIFITVNTYHNSG 117  
QY 117 LYTCNVSREFEFAHRPFVKTTRLLPLRVTAEAGDEFTSVSEIMTYLLVFLTMLEFIE 176  
DB 118 DYQCHVYRLSFEYENHTSVYKKIHLEVDKARDMASIVSEIMTYLLVFLTMLEFIE 177  
QY 177 MIYCYRKYKA-EBAQENASDYLAIPSENKEN 208  
DB 178 MVIYCYKIAAATBAQENASEYLAIPSENKEN 210

## RESULT 11

US-10-142-201B-8  
; Sequence 8, Application US/10142201B  
; Publication No. US20030022205A1  
; GENERAL INFORMATION:

; APPLICANT: Millenium Pharmaceuticals Inc.  
; TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,  
; FILE REFERENCE: MP12001-106P1R(M)  
; CURRENT APPLICATION NUMBER: US/10/142, 201B  
; PRIOR FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: US 60/289,893  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-142-201B-8

Query Match 41.5%; Score 466.5; DB 14; Length 218;  
Best Local Similarity 51.6%; Pred. No. 9.8e-39;  
Matches 98; Conservative 28; Mismatches 57; Indels 7; Gaps 4;

QY 26 CVEVPSSETEAVOGNPMKLRICSCMKREVEATTVVEMFPRGGKDFLIYENRNGHOV 84  
DB 21 CVEVDSSETEAVOGNPMKLRICSCMKREVEATTVVEMFPRGGKDFLIYENRNGHOV 80  
QY 85 ESP--FGRLQWNGS--KDLOVSIITVNTLNDGLYTCNVSREFEFAHRPFVKTTR 139  
DB 81 EDERFEGRVVWNGSRGTKDLOLSIFITVNTYHNSGDECHVYRLLEFVYENHTSVYK 140  
QY 140 LPLRVTAEAGDEFTSVSEIMTYLLVFLTMLEFIEIMTYCYRKYKA-EBAQENASDY 198  
DB 141 KIHIEVDKARDMASIVSEIMTYLLVFLTMLEFIEIMTYCYRKYKA-EBAQENASDY 200  
QY 199 LAIPSENKEN 208  
DB 201 LAIPSENKEN 210

## RESULT 12

US-10-477-272-2  
; Sequence 2, Application US/10477272  
; Publication No. US20040191791A1  
; GENERAL INFORMATION:



APPLICANT: Bionomics Limited  
TITLE OF INVENTION: P12  
FILE REFERENCE: SCNB (P85C)  
CURRENT APPLICATION NUMBER: US/10/477,272  
CURRENT FILING DATE: 2003-11-10  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-477-272-2

Query Match 41.5%; Score 466.5; DB 16; Length 218;  
Best Local Similarity 51.6%; Pred. No. 9.8e-39;  
Matches 98; Conservative 28; Mismatches 57; Indels 7; Gaps 4;

QY 26 CVEVPESTEAVQGNPMKLRICISCKREVEATTVVEMFYRPEGKDFL-IYERYNGHOEV 84  
DB 21 CVEVDETEAVVGMTEFKILCISCKRSEETAETFTETFRQKTEEFVKILRYENEVLQ 80  
QY 85 ESP--FOGRLOWNGS--KLDVSTVLTNLTNDGSLTYCNVSRFEFFAHRPFVKTTR 139  
DB 81 EDECEGEGRVVWNGSGTKDLDLSIFITVTVNHSGDYCHYRLLFFENYEHTNSVVK 140  
QY 140 LIPLRVTEAGEDEFTSVSEIMMYILLVPLTLMFLIEMIYCYRKVSKA--EAAQENASDY 198  
DB 141 KIHIEVVDKANRMASIVSEIMMYILLVPLTLMVAMMIYCYKIAAATETAQENASEY 200

QY 199 LAIPSENKEN 208  
DB 201 LAITSESKEN 210

RESULT 13  
US-09-977-579-44  
Sequence 44; Application US/0977579  
Publication No. US20040248240A1  
GENERAL INFORMATION:  
APPLICANT: Cambridge University Technical Services  
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod  
TITLE OF INVENTION: channel  
TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t  
FILE REFERENCE: 674558-2001  
CURRENT APPLICATION NUMBER: US/09/977,579  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: PCT/EP00/01783  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60,129,473  
PRIOR FILING DATE: 2000-02-24  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 44  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Rat  
US-09-977-579-44

Query Match 41.2%; Score 463.5; DB 11; Length 218;  
Best Local Similarity 51.1%; Pred. No. 2e-38;  
Matches 97; Conservative 29; Mismatches 57; Indels 7; Gaps 4;

QY 26 CVEVPESTEAVQGNPMKLRICISCKREVEATTVVEMFYRPEGKDFL-IYERYNGHOEV 84  
DB 21 CVEVDETEAVVGMTEFKILCISCKRSEETAETFTETFRQKTEEFVKILRYENEVLQ 80  
QY 85 ESP--FOGRLOWNGS--KLDVSTVLTNLTNDGSLTYCNVSRFEFFAHRPFVKTTR 139  
DB 81 EDEBEREGRVVWNGSGTKDLDLSIFITVTVNHSGDYCHYRLLFFENYEHTNSVVK 140  
QY 140 LIPLRVTEAGEDEFTSVSEIMMYILLVPLTLMFLIEMIYCYRKVSKA--EAAQENASDY 198  
DB 141 KIHIEVVDKANRMASIVSEIMMYILLVPLTLMVAMMIYCYKIAAATETAQENASEY 200

QY 199 LAIPSENKEN 208  
DB 201 LAITSESKEN 210

RESULT 14  
US-10-029-191-7  
Sequence 7; Application US/10029191  
Publication No. US20020160453A1  
GENERAL INFORMATION:  
APPLICANT: CURTIS, ROY A. J.  
TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL, BETA-3 SUBUNIT  
FILE REFERENCE: 210147.00XX/5U1  
CURRENT APPLICATION NUMBER: US/10/029,191  
CURRENT FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 09/569,978  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/134,198  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-10-029-191-7

Query Match 26.0%; Score 292; DB 13; Length 58;  
Best Local Similarity 100.0%; Pred. No. 7.2e-22;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 SEIMMYILLVPLTLMFLIEMIYCYRKVSKAEEAQAQENASDYLAIPSENKENVVPEE 215  
DB 1 SEIMMYILLVPLTLMFLIEMIYCYRKVSKAEEAQAQENASDYLAIPSENKENVVPEE 58

RESULT 15  
US-09-875-456A-14  
Sequence 14; Application US/09875456A  
Patent No. US20020045229A1  
GENERAL INFORMATION:  
APPLICANT: Qtn, Ning  
APPLICANT: Codd, Ellen  
APPLICANT: D'Andrea, Michael  
TITLE OF INVENTION: DNAs encoding human beta1a sodium channel subunit  
FILE REFERENCE: ORT-1221  
CURRENT APPLICATION NUMBER: US/09/875,456A  
CURRENT FILING DATE: 2001-09-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 268  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-875-456A-14

Query Match 22.9%; Score 257.5; DB 9; Length 268;  
Best Local Similarity 44.7%; Pred. No. 1.7e-17;  
Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

QY 26 CVEVPESTEAVQGNPMKLRICISCKREVEATTVVEMFYRPEGKDFL-IYERYNGHOEV 84  
DB 21 CVEVDETEAVVGMTEFKILCISCKRSEETAETFTETFRQKTEEFVKILRYENEVLQ 80  
QY 85 ESP--FOGRLOWNGS--KLDVSTVLTNLTNDGSLTYCNVSRFEFFAHRPFVKTTR 139  
DB 81 EDEBEREGRVVWNGSGTKDLDLSIFITVTVNHSGDYCHYRLLFFENYEHTNSVVK 140  
QY 140 LIPLRVTEAGE 151  
DB 141 KIHIEVVDK-GE 151

Search completed: March 31, 2005, 20:39:32  
Job time : 92.5 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:10:33 ; Search time 26.5 Seconds

(without alignments)  
780.627 Million cell updates/sec

Title: US-09-977-579-1

Perfect score: 1125

Sequence: 1 MPAFNRLPLASLVLYWVR.....SDYLAIPEKENVVPEE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:\*

2: PIR1:\*

3: PIR2:\*

4: PIR3:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	470.5	41.8	218	2 UC4788	sodium channel pro
2	466.5	41.5	218	2 A55734	sodium channel, vo
3	463.5	41.2	218	2 A42737	sodium channel bet
4	168	14.9	248	1 MPRT0	myelin P0 protein
5	164	14.6	248	1 JH0252	myelin P0 protein
6	164	14.6	251	2 I38053	myelin protein zer
7	162	14.4	219	1 A29128	myelin P0 protein
8	147.5	13.1	247	1 A54662	myelin P0 protein
9	145.5	12.9	246	1 A32999	myelin P0 protein
10	136	12.1	249	1 A61087	myelin P0 glycopro
11	113	10.0	215	2 A57843	sodium channel bet
12	112	10.0	186	2 I61783	sodium channel bet
13	109.5	9.7	1462	1 B36182	protein-tyrosine-p
14	107.5	9.6	820	2 S17295	fibroblast growth
15	107.5	9.6	821	1 TVMGBK	fibroblast growth
16	106	9.4	800	1 TVHUF2	fibroblast growth
17	104	9.2	800	2 A48991	heparin-binding gr
18	104	9.2	801	2 I55363	heparin-binding gr
19	102.5	9.1	131	2 PT0178	ig kappa chain pre
20	101.5	9.0	129	2 S57884	ig kappa chain pre
21	101.5	9.0	131	2 B32513	ig kappa chain pre
22	101.5	9.0	131	2 B30577	ig kappa chain pre
23	101.5	9.0	353	2 S51242	heparin-binding fi
24	100.5	8.9	118	2 S24539	ig kappa chain V r
25	100.5	8.9	131	2 D34904	ig kappa chain pre
26	99.5	8.8	131	2 S24533	ig kappa chain V r
27	98.5	8.8	131	2 B39276	ig light chain pre
28	98.5	8.8	806	2 A35963	protein-tyrosine k
29	98	8.7	130	2 C29380	ig kappa chain pre

30	98	8.7	372	2 C39371	ig V-region-like B
31	97	8.6	136	2 S36320	T-cell receptor de
32	96.5	8.6	118	2 S24535	ig kappa chain V r
33	96.5	8.6	118	2 S24500	ig kappa chain V r
34	96.5	8.6	118	2 S24529	ig kappa chain V r
35	96.5	8.6	131	2 B34904	ig kappa chain pre
36	96.5	8.6	131	2 S09259	ig kappa chain pre
37	95.5	8.5	118	2 S24507	ig kappa chain V r
38	95.5	8.5	132	2 PH0106	anti-digoxin trans
39	95.5	8.5	750	2 S41051	fibroblast growth
40	95.5	8.5	821	1 TVHUF2	fibroblast growth
41	95.5	8.5	898	2 A40114	fasciclin II precu
42	94.5	8.4	118	2 S24536	ig kappa chain V r
43	94.5	8.4	118	2 S24503	ig kappa chain V r
44	94.5	8.4	118	2 S24508	ig kappa chain V r
45	94.5	8.4	118	2 S24532	ig kappa chain V r

## ALIGNMENTS

### RESULT 1

sodium channel protein betal chain - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 10-May-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C/Accession: UC4788

A:Title: Cloning of the cDNA encoding the sodium channel betal subunit from rabbit.

A/Reference number: UC4788; PMID:9625151; PMID:8666261

A/Accession: UC4788

A/Molecule type: mRNA

A/Residues: 1-218 <BEL>

A/Cross-references: UNIPROT:P53788; GB:U35382; NID:G1016013; PIDN:AAB17572.1; PID:G1016013

C/Comment: This protein is composed of a large alpha-chain and two small beta-chains and

duction.

C/Genetics:

A/Gene: Obetal

C/Keywords: glycoprotein; membrane protein; muscle; transmembrane protein

F;161-182/Domain: transmembrane #status predicted <TM>

F;93,110,114,135/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 41.8%; Score 470.5; DB 2; Length 218;

Best Local Similarity 49.3%; Pred. No. 5.8e-34;

Matches 105; Conservative 29; Mismatches 64; Indels 15; Gaps 6;

Qy	6	RLPL--ASLVLIYWRVCFPVCEVPSFETAVVQGNPKLRICSCMKREVEATTVVEM	62
Db	3	RLAFAVVGALVSSAM---GGCEVDSETEAVYGTFTKILCICGRSETTAETTEW	57
Qy	63	FYPBEGKDFL-IYERNQHVEESP--FOGRLOMNGS--KDLQDVSTLVNLTNDG	116
Db	58	TFQKGTBEFVKILRYENEVLQLEBDEPRGKRVVNGSRETQLODLSITVTWYHSG	117
Qy	117	LYTCNVSRPEFPAHPPFKYTRLLPLRYTEEGEFTSVSGIMVILVFLTWFIE	176
Db	118	DYQCHVYRLLSFENYHNTSVVKRIHLEVVDKKNRMWASISIMYVLTIVLTVLVAE	177
Qy	177	MYCYRVSKA--EAAQENASDYLAIPESEKEN	208
Db	178	MYCYKIKIAATAAQAENASEYLAIITSEKEN	210

### RESULT 2

sodium channel, voltage-gated, beta-1 chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004

C/Accession: A55734; A53408; I54354

R/Makita, N.; Sloan-Brown, K.; Weghuis, D.O.; Rogers, H.H.; George Jr., A.L.

Genomics 23, 628-634, 1994

A/Title: Genomic organization and chromosomal assignment of the human voltage-gated Na(+)

A:Reference number: A55734; MUID:95154833; PMID:7851891  
A:Accession: A55734  
A:Molecule type: DNA  
A:Residues: 1-218 <MAX1>  
A:Cross-references: UNIPROT:O07699; GB:U12189  
R.Makita, N.; Bennett Jr., P.B.; George Jr., A.L.  
J. Biol. Chem. 269, 7571-7578, 1994  
A:Title: Voltage-gated Na(+) channel beta-1 subunit mRNA expressed in adult human skeletal muscle  
A:Reference number: A53408; MUID:94171787; PMID:8125980  
A:Accession: A53408  
A:Molecule type: mRNA  
A:Residues: 1-218 <MAX2>  
A:Cross-references: GB:LI6242; NID:g450602; PIND:AAA61277.1; PID:g450603  
R.McLachley, A.L.; Cannon, S.C.; Slaugenhaupt, S.A.; Gusella, J.F.  
Hum. Mol. Genet. 2, 745-749, 1993  
A:Title: The cloning and expression of a sodium channel beta 1-subunit cDNA from human brain  
A:Reference number: I54354; MUID:93357746; PMID:8394762  
A:Accession: I54354  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-218 <RES>  
A:Cross-references: GB:LI0338; NID:g307414; PIND:AAA60391.1; PID:g307415  
A:GeneticS:  
A:Gene: GDB:SCN1B  
A:Cross-references: GDB:127281; OMIM:600235  
A:Map position: 19q13.1-19q13.1  
A:Keywords: glycoprotein; muscle; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:161-182/Domain: transmembrane #status predicted <TM>  
F:193-110,114,135/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	41.5%	Score 466.5;	DB 2;	Length 218;
Best Local Similarity	51.6%;	Pred. No. 1.3e-33;		
Matches 98;	Conservative 28;	Mismatches 57;	Indels 7;	Gaps 4;

[illegible]

RESULT 3  
A42737  
sodium channel beta 1 subunit - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A42737  
R/Isom: L.L.; De Jongh, K.S.; Patton, D.E.; Rebert, B.F.; Offord, J.; Charbonneau, H.; Wang, S.  
Science 256, 839-842, 1992  
A/Title: Primary structure and functional expression of the beta 1 subunit of the rat brain sodium channel  
A/Reference number: A42737; MUID:92271207; PMID:1375395  
A/Accession: A42737  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid; protein  
A/Residues: 1-218 <150>  
A/Cross-references: UNIPROT:000954; GB:M91808; NID:9206864; PIDN:AAA8513.1; PID:g206865  
A/Experimental source: brain  
A/Note: sequence extracted from NCBI backbone (NCBI:P:103298)  
/Keywords: transmembrane protein

Query Match	41.2%;	Score 463.5;	DB 2;	Length 218;
Best Local Similarity	51.1%;	Pred. No. 2.4e-33;		

Matches	97; Conservative	29; Mismatches	57; Indels	7; Gaps	4;
QY	26	CVEPSETEAVOGNPMKLRICISCMKREEVEATTVMFVPEGGKDFL-ITYEYNGHOEV	84		
Db	21	CVEVSETEAVVGMFVKILICISCKRSEETAEFTFTWTFROKTEEFVKILIRENEVQL	80		
QY	85	ESP--FQGRLOWNGS---WDLDVSTVLTNVLNDSGLYCNVSRREFEFAHRFVFKTR	139		
Db	81	EDEFEREGVWVNGSGTYLDPLSIFITNVTYNHSGDYCHVYRLLPDYEHNTSVVK	140		
QY	140	LIPRLVTEAGADFTSVSEIMMYILVFLTLVLFLEMICYRKVSKA-EEAAGENSADY	198		
Db	141	KIHLEVDKANDMASIVSEIMMYVILVLTITLVAMVYCYKXIAATEAAAGENSSEY	200		
QY	199	LAIPSENKEN 208			
Db	201	LAITSESKEN 210			
RESULT 4					
MERTO					
myelin P0 protein precursor - rat					
C.Species: Rattus norvegicus (Norway rat)					
C.Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #ext_change 09-Jul-2004					
C.Accession: J00622; A22822					
R.Lemke, G.; Lamar, E.; Patterson, J.					
Neuron 1, 73-83, 1988					
A.Title: Isolation and analysis of the gene encoding peripheral myelin protein zero.					
A.Reference number: J00622; MUID:90166482; PMID:2483091					
A.Accession: J00622					
A.Molecule type: DNA					
A.Residues: 1-248 <LEM>					
A.Cross-references: UNIPROT: P06907					
R.Lemke, G.; Axel, R.					
Cell 40, 501-508, 1985					
A.Title: Isolation and sequence of a cDNA encoding the major structural protein of perip					
A.Reference number: A22822; MUID:85124601; PMID:2578885					
A.Accession: A22822					
A.Molecule type: mRNA					
A.Residues: 1-248 <LEM2>					
C.Comment: This protein is found only in peripheral nervous system Schwann cells.					
C.Genetics:					
A.Introns: 23/1, 78/3, 150/1, 195/2, 215/3					
C.Subfamily: myelin P0 protein; immunoglobulin homology					
C.Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protein					
F.1-29/Domain: signal sequence #status predicted <SIG>					
F.30-248/Product: myelin P0 protein #status predicted <MAT>					
F.30-153/Domain: extracellular #status predicted <EXD>					
F.43-129/Domain: immunoglobulin homology <IMM>					
F.154-179/Domain: transmembrane #status predicted <TMD>					
F.180-248/Domain: intracellular #status predicted <IND>					
F.122/Binding site: carbohydrate (Asn) (covalent) #status predicted					
Query Match 14.9%; Score 168; DB 1; Length 248;					
Best Local Similarity 27.2%; Pred. No. 2, 3e-07;					
Matches 58; Conservative 35; Mismatches 102; Indels 18; Gaps 7;					
QY	8	LPLASLVIIVWVRCPCVEVSETEAVOGNPMKLRICISCMKREEVEATTVMFVPE	67		
Db	17	LIFSSLVLT---SPLTIAVVTYDREYVGAAGSVTLTLC-SFWSSEWVSDISFTWRYQPE	71		
QY	68	GGKDL-ITYEYNGHOEV--SPFQGRLOWNGSKLDQVSIITLVNLTNDSGLTYCNVSR	124		
Db	72	GGRDALISFHVAKGQYIDVGVGFKERIQWGDGSPSKMDSIVIHNDYSDNGTTCVKN	131		
QY	125	EFEFAHRPFVTKTRLIPLRVTEAGADFTSVSEIMMYIL-LVFLTLVLFLEMICYRK	183		
Db	132	PPD-----IVGKTSQVTLVFEKVPFTRGVVGAIVGILVTLTLFYLIRYCMWR	185		
QY	184	VSKAE---AAQENASDYLAIPSENKENSVPV 213			
Db	186	ROAALQORLSAMEKGFHKSSKDDSSKRGQTPV 218			

Db 186 RQAAIQRRLSAMEKGFHKSSKDSKRGQTPV 218

Db 186 RQALQRLSMEKGFHKSSKDSKRGQTPV 218

## RESULT 5

JH0252

myelin P0 protein precursor - human

N/Alternate names: myelin protein zero

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence, revision 06-Dec-1996 #text\_change 09-Jul-2004

C/Accession: JH0252; JN0704; I39378; I58118

R/Hayasaka, K.; Nanno, K.; Tahara, M.; Sato, W.; Takada, G.; Mura, M.; Uemura, K.

Biochem. Biophys. Res. Commun. 180, 515-518, 1991

A/Title: Isolation and sequence determination of cDNA encoding the major structural prot

A/Reference number: JH0252; PMID:92062068; PMID:171967

A/Accession: JH0252

A/Molecule type: mRNA

A/Residues: 1-248 &lt;HA&gt;

A/Cross-references: UNIPROT:P25188; GB:D10537; GB:D90501; NID:94220073; P1DN:BA01395.1;

A/Experimental source: fetus spinal cord

R/Hayasaka, K.; Ohnishi, A.; Takada, G.; Fukushima, Y.; Mura, Y.

Biochem. Biophys. Res. Commun. 194, 1317-1322, 1993

A/Title: Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy type 1.

A/Reference number: JN0704; PMID:9356807; PMID:7668964

A/Accession: JN0704

A/Molecule type: mRNA

A/Residues: 1-248 &lt;HA2&gt;

R/Pham-Dinh, D.; Fourbl, Y.; Blanquet, F.; Mattei, M.G.; Roeckel, N.; Latour, P.; Chaz

Hum. Mol. Genet. 2, 2051-2054, 1993

A/Title: The major peripheral myelin protein zero gene: structure and localization in th

A/Reference number: I39378; PMID:94154677; PMID:7509228

A/Accession: I39378

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-248 &lt;RES&gt;

A/Cross-references: GB:I24893; NID:9454412; P1DN:AAA20656.1; P1D:9529405

R/Kulkarni, T.; Bolhuis, P.A.; Wolterman, R.A.; Kemp, S.; de Nijhuis, S.; Valentijn, L.

Nature Genet. 5, 35-39, 1993

A/Title: Deletion of the serine 34 codon from the major peripheral myelin protein P0 ge

A/Reference number: I58118; PMID:94053114; PMID:7693130

A/Accession: I58118

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-62, 64-115 &lt;RES2&gt;

A/Cross-references: GB:S66705; NID:9437048; P1DN:AA28708.1; P1D:9437049

A/Experimental source: disease-state mutant

C/Comment: This protein, a small integral membrane glycoprotein, is the most abundant pr

C/Comment: This protein plays essential roles in both the elaboration and the subsequent

C/Accession: GDB:MP2; CMT1B; CMT1B; HMSNIB

A/Cross-references: GDB:125266; OMIM:159440

A/Map position: 1q22-1q23

A/Intons: 23/1; 78/3; 150/1; 195/2; 215/3

C/Superfamily: myelin P0 protein; immunoglobulin homology

C/Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein

F/1-29/Dominant: signal sequence #status predicted &lt;SIG&gt;

F/30-248/Product: peripheral myelin #status predicted &lt;PER&gt;

F/43-129/Dominant: immunoglobulin homology &lt;IMM&gt;

F/50-127/Dissulfide bonds: #status predicted

F/122/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 164; DB 1; Length 248;

Best Local Similarity 27.7%; Pred. No. 5.2e-07;

Matches 53; Conservative 34; Mismatches 82; Indels 22; Gaps 7;

14 VLIYWRVCFP---VCVEVSETEAVOAGNPMKRCISCMKEVEATVTVEMFYRPEGK 70

16 VLFSSLVSPAPAIYVYTDREHVGAVGSRVTLHC-SFMSSEVAVSDISFTWRYOPEGGR 74

71 DFL-IYEYRNGHQEVE--SPFGRLQWNGSKDLQDVSIYLVNTLNDSGLYTCNVSEPE 127

75 DAISIFHYAKGQYIDVGVGFKERIQWVGPBPKMKGSIYVHNLDYSDNGFTCDVKNPPD 134

128 FEARFPVKTRTLPLRVTEAGEDFTSVSEIMMTYL-LVFLTLMLFIMICY-----181

135 -----IVGTSQVTLVYFEKVPTRVGVVVGAVIGVLLVLLLLFFVVRVCMRLRQA 188

## RESULT 6

myelin protein zero - human

C/Species: Homo sapiens (man)

C/Date: 17-May-1996 #sequence, revision 17-May-1996 #text\_change 09-Jul-2004

C/Accession: I38053; A49643; S43191

R/Rautenstrauss, B.; Nellis, E.; Gehl, H.; Pfeiffer, R.A.; Van Broeckhoven, C.

Hum. Mol. Genet. 3, 1701-1702, 1994

A/Title: Identification of a de novo inactivating mutation in P0 in a patient with a Dejer

A/Reference number: I38053; PMID:95135435; PMID:7530550

A/Accession: I38053

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-251 &lt;RES&gt;

A/Cross-references: UNIPROT:Q14902; EMBL:Z31718; NID:9469516; P1DN:CAA83513.1; P1D:946951

R/Su, Y.; Brooks, D.G.; Li, L.; Lepercq, J.; Trofatter, J.A.; Ravetch, J.V.; Lebo, R.V.

Proc. Natl. Acad. Sci. U.S.A. 90, 10856-10860, 1993

A/Title: Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B patients.

A/Reference number: A49643; PMID:94068501; PMID:7504284

A/Accession: A49643

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 50-105 &lt;SU1&gt;

A/Experimental source: peripheral blood

A/Note: sequence extracted from NCBI backbone (NCBIP:139777)

C/Genetics:

A/Gene: GDB:MP2; CMT1B; CMT1

A/Cross-references: GDB:125266; OMIM:159440

A/Map position: 1q22-1q23

C/Superfamily: myelin P0 protein; immunoglobulin homology

F/43-129/Dominant: immunoglobulin homology &lt;IMM&gt;

Query Match 14.6%; Score 164; DB 2; Length 251;

Best Local Similarity 27.7%; Pred. No. 5.2e-07;

Matches 53; Conservative 34; Mismatches 82; Indels 22; Gaps 7;

14 VLIYWRVCFP---VCVEVSETEAVOAGNPMKRCISCMKEVEATVTVEMFYRPEGK 70

16 VLFSSLVSPAPAIYVYTDREHVGAVGSRVTLHC-SFMSSEVAVSDISFTWRYOPEGGR 74

71 DFL-IYEYRNGHQEVE--SPFGRLQWNGSKDLQDVSIYLVNTLNDSGLYTCNVSEPE 127

75 DAISIFHYAKGQYIDVGVGFKERIQWVGPBPKMKGSIYVHNLDYSDNGFTCDVKNPPD 134

128 FEARFPVKTRTLPLRVTEAGEDFTSVSEIMMTYL-LVFLTLMLFIMICY-----181

135 -----IVGTSQVTLVYFEKVPTRVGVVVGAVIGVLLVLLLLFFVVRVCMRLRQA 188

182 ---RKVSKAE 189

189 ALQRLSAMEK 199

## RESULT 7

myelin P0 protein - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: A29128

R/Sakamoto, Y.; Kitamura, K.; Yoshimura, K.; Nishijima, T.; Uemura, K.

J. Biol. Chem. 262, 4208-4214, 1987

A/Title: Complete amino acid sequence of P0 protein in bovine peripheral nerve myelin.

A/Reference number: A29128; PMID:87166035; PMID:2435734

A/Accession: A29128

A/Molecule type: protein

A/Residues: 1-219 &lt;SAK&gt;

A/Cross-references: UNIPROT:P10522



QY 194 NASD 197  
Db 205 SAKD 208

## RESULT 11

A57843  
sodium channel beta 2 subunit - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: A57843  
R/Isom: L.L.; Ragsdale, D.S.; DeJonigh, K.S.; Westenhoeck, R.E.; Reber, B.F.X.; Scheuer, C.  
Cell 83, 433-442, 1995  
A/Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transmembrane Protein  
A/Reference number: A57843; PMID:96067641; PMID:8521473  
A/Accession: A57843  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-215 <RES>  
A/Cross-references: UNIPROT:P54900; EMBL:U37026; NID:g1086496; PIDN:AA052967.1; PID:g1086496  
C/Genetics:  
A/Gene: SCN2

Query Match 10.0%; Score 113; DB 2; Length 215;  
Best Local Similarity 25.3%; Pred. No. 0.013;  
Matches 47; Conservative 39; Mismatches 80; Indels 20; Gaps 8;

QY 27 VEVPSSTBAVQGNPMKLRCT--SCMKREVEATTVMFPRPGG--KQFLIYRNGH 81  
Db 32 VIVPTLTVANGSDTRLPCTFNHCYVNHQFS--LMTVQECSCSEMFLOPRMKIIN 89  
QY 82 OEVEPSFQRLONGSKDLDVSIIVLNTLNDGLTCNVSEFEFAHRPFVKTTRLI 141  
Db 90 LKLER-FGDRVERSGNPSKIDVSVTLKNVQLEDEGINCTIN--PPDRHGHGK---1 142  
QY 142 PLRVTEAGEDFTSVSEIMVILVFLTLMEFLIEMV-CYRKVSKAEAAQENASDYLA 200  
Db 143 YLQVLLVPPERDSTVAIVGASVGFLLAVIILVMVKKVRR-----KKEQLSTDDK 197  
QY 201 IPSENK 206  
Db 198 TEEEGK 203

## RESULT 12

161783  
sodium channel beta 2 subunit - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I61783  
R/Isom: L.L.; Ragsdale, D.S.; DeJonigh, K.S.; Westenhoeck, R.E.; Reber, B.F.X.; Scheuer, C.  
Cell 83, 433-442, 1995  
A/Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transmembrane Protein  
A/Reference number: A57843; PMID:96067641; PMID:8521473  
A/Accession: I61783  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-186 <RES>  
A/Cross-references: UNIPROT:Q62861; EMBL:U37147; NID:g1086498; PIDN:AA060506.1; PID:g1086498  
C/Genetics:  
A/Gene: SCN2  
A/Introns: 50/3; 120/2

Query Match 10.0%; Score 112; DB 2; Length 186;  
Best Local Similarity 24.1%; Pred. No. 0.014;  
Matches 47; Conservative 36; Mismatches 74; Indels 38; Gaps 8;

QY 27 VEVPSSTBAVQGNPMKLRCT--SCMKREVEATTVMFPRPGGKDFLIYRNGH 84  
Db 3 VIVPTLTVANGSDTRLPCTFNHCYVNHQFS--LMTVQ-----ECSCSEEM 50  
QY 85 EEPFQ-----GRLQNGSKDLDVSIIVLNTLNDGLTCNVSEFEFAHR 132

Db 51 VLQPRMKIINKLEREGDRVEFGNPSKYDVSTLKNVQLEDEGINCYITN--PPDRHR 108  
QY 133 PFVKTTRLPLKTEBAGEFTSVSEIMVILVFLTLMEFLIEMV-CYRKVSKAEAA 191  
Db 109 GHGK---YLQVLLVPPERDSTVAIVGASVGFLLAVIILVMVKKVRR-----KKE 159  
QY 192 QENASDYLAIPSENK 206  
Db 160 QKSTDDKTEEGK 174

## RESULT 13

B36182  
N-tyrosine-phosphatase (EC 3.1.3.48), receptor type PTP69D precursor - fruit fly (Drosophila melanogaster)  
C/Species: Drosophila melanogaster  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: B36182  
R/Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989  
A/Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila  
A/Reference number: A36182; PMID:90046860; PMID:2554325  
A/Accession: B36182  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-1462 <STR>  
A/Cross-references: UNIPROT:P16620; GB:M27699; NID:g158188; PIDN:AAA28842.1; PID:g158188  
C/Genetics:  
A/Gene: PTP69D  
A/Cross-references: FlyBase:FBgn014007  
C/Superfamily: protein-tyrosine-phosphatase, receptor type PTP69D; fibronectin type III; phosphatase homology  
C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; signal sequence; status predicted <SIG>  
F/1-28/Domain: protein-tyrosine-phosphatase, receptor type PTP69D #status predicted <EXT>  
F/29-806/Domain: extracellular #status predicted <EXT>  
F/38-114/Domain: immunoglobulin homology <IM1>  
F/147-216/Domain: immunoglobulin homology <IM2>  
F/807-823/Domain: transmembrane #status predicted <TM>  
F/824-1462/Domain: intracellular #status predicted <INT>  
F/917-1145/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F/1213-1439/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F/45-112,154-214/Disulfide bonds: #status predicted  
F/1097/Active site: Cys (phosphocysteine intermediate) #status predicted  
F/1103/Binding site: substrate phosphate (Arg) #status predicted  
F/1391/Active site: Cys (phosphocysteine intermediate) #status predicted  
F/1397/Binding site: substrate phosphate (Arg) #status predicted

Query Match 9.7%; Score 109.5; DB 1; Length 1462;  
Best Local Similarity 26.7%; Pred. No. 0.22;  
Matches 47; Conservative 31; Mismatches 61; Indels 37; Gaps 11;

QY 4 FNNLLPLASIVLIVYVFCVCEVSETE-AVQGNPMKLRCTSCMKREVEATTVM 62  
Db 5 YRMSMLNIIILAY-IFLC-AICVQSVGQWAEIKNVSLEAS-----ENNA---VAV 54  
QY 63 FYRPEG-GKDFLIYRNGHGEVESFQRLONGSKDLDVSIIVLNTLNDGL 116  
Db 55 KLGNQITINKNHPFYKIRT-----EPLKNDGSENNDQDFMKYKNVTLTLDVNTDNG 108  
QY 117 LYTC-----NYSREFEFAHRPFVKTTRLIPLRVTEAGEDFTSVSEIMVIL 166  
Db 109 NYCTAQTQGNHSTEFQVRYLP-SKVLQSTPDRIRKIKQD-----VMLYCL 156

## RESULT 14

S17295  
fibroblast growth factor receptor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S17295  
R/Raz, V.; Kellman, Z.; Avioli, A.; Neufeld, G.; Givol, D.; Yarden, Y.  
Oncogene 6, 753-760, 1991

A>Title: PCR-based identification of new receptors: molecular cloning of a receptor for  
A:Reference number: S17295; MUID:91270892; PMID:1711190  
A:Accession: S17295  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-820 <RAZ>  
A:Cross-references: UNIPROT:P21803; EMBL:X55441; NID:G50141; PID:CAA39083.1; PID:G50142  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
F:270-343/Domain: immunoglobulin homology <IMM>  
F:478-763/Domain: protein kinase homology <KIN>

Query Match 9.6%; Score 107.5; DB 2; Length 820;  
Best Local Similarity 25.9%; Pred. No. 0.17;  
Matches 41; Conservative 22; Mismatches 56; Indels 39; Gaps 7;

QY 83 EVESPFQGRLOW-----NGSK-----DLDVSIYV---NVTLNDG 116  
DB 278 KYSDAQPHIQWKVEKNGSKYGPDLPLKVLKAAGVNTTDEKEIVLYIRNVTFFEDAG 337  
QY 117 LYTGVNSREFEFEARHPVKTRRLPLRVTE-EAGEDFTSVSEIMMYILLVFLTLMFLI 175  
DB 338 EYTCLAGNSIGISFHSAML-TVLPAPVREKEITASPDYL---ETAIYICIGVFLIACMV 392  
QY 176 EMICYRKVSKAEBAQENASDYLAIPSENKENSVPV 213  
DB 393 TVIFCRMKTTTK-----PDFSSQPAVHKLTRIPL 423

## RESULT 15

TVMSBK  
fibroblast growth factor receptor bek precursor - mouse  
N:Alternate names: bek transforming protein; fibroblast growth factor receptor 2; kerati  
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) bek  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1991 #sequence revision 13-Mar-1997 #text change 09-Jul-2004  
C:Accession: A41142; A31378  
R:Mansukhani, A.; Dell'Era, P.; Moscatelli, D.; Kornbluth, S.; Hanafusa, H.; Basilio, C  
Proc. Natl. Acad. Sci. U.S.A. 89, 3305-3309, 1992  
A>Title: Characterization of the murine BEK fibroblast growth factor (FGF) receptor: act  
A:Reference number: A41142; MUID:92228773; PMID:1373495  
A:Accession: A41142  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-821 <MAN>  
A:Cross-references: UNIPROT:P21803; GB:M86441  
R:Kornbluth, S.; Paulson, K.E.; Hanafusa, H.  
Mol. Cell. Biol. 8, 5541-5544, 1988  
A>Title: Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA  
A:Reference number: A31378; MUID:89219016; PMID:2468999  
A:Accession: A31378  
A:Molecule type: mRNA  
A:Residues: 477-821 <KOR>  
A:Cross-references: GB:M23362; NID:G533219; PIDN:AAA37285.1; PID:G533220  
C:Genetics:  
A:Gene: bek  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:122-821/Product: fibroblast growth factor receptor bek #status predicted <MAT>  
F:117-233/Domain: immunoglobulin homology <IMM>  
F:378-398/Domain: transmembrane #status predicted <TM>  
F:479-764/Domain: protein kinase homology <KIN>  
F:487-495/Region: protein kinase ATP-binding motif  
F:62-107,179-231,278-342/Dissulfide bonds: #status predicted  
F:83,123,147,241,265,297,318,331/Binding site: carbohydrate (asn) (covalent) #status pre  
F:517,534,626/Active site: Lys, Glu, Asp #status predicted  
F:657/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 9.6%; Score 107.5; DB 1; Length 821;

Best Local Similarity 25.9%; Pred. No. 0.17;  
Matches 41; Conservative 22; Mismatches 56; Indels 39; Gaps 7;

QY 83 EVESPFQGRLOW-----NGSK-----DLDVSIYV---NVTLNDG 116

DB 279 KYSDAQPHIQWKVEKNGSKYGPDLPLKVLKAAGVNTTDEKEIVLYIRNVTFFEDAG 338  
QY 117 LYTGVNSREFEFEARHPVKTRRLPLRVTE-EAGEDFTSVSEIMMYILLVFLTLMFLI 175  
DB 339 EYTCLAGNSIGISFHSAML-TVLPAPVREKEITASPDYL---ETAIYICIGVFLIACMV 393  
QY 176 EMICYRKVSKAEBAQENASDYLAIPSENKENSVPV 213  
DB 394 TVIFCRMKTTTK-----PDFSSQPAVHKLTRIPL 424

Search completed: March 31, 2005, 20:22:48  
Job time : 28.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:02:27 ; Search time 116 seconds  
(without alignments) 949.112 Million cell updates/sec

Title: US-09-977-579-1

Perfect score: 1125

Sequence: 1 MPAPFRLPLASLVLYWVR.....SDYLAIPEKSNKSVVPEE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1125	100.0	215	1	CIB3_RAT	09jko0 rattus norv
2	1117	99.3	215	1	CIB3_MOUSE	08bhz2 mus musculu
3	1117	99.3	268	2	069203	0892q3 mus musculu
4	1105	98.2	215	1	CIB3_HUMAN	09ny72 homo sapien
5	1097	97.5	215	1	CIB3_MACFA	08hx77 macaca fasc
6	700	62.2	215	2	06DE47	06de47 xenopus lae
7	470.5	41.8	218	1	CIB1_RABIT	P53788 oryctolagus
8	466.5	41.5	218	1	CIB1_HUMAN	007699 homo sapien
9	463.5	41.2	218	1	CIB1_RAT	000954 rattus norv
10	461	41.0	218	1	CIB1_MOUSE	P97952 mus musculu
11	419.5	37.3	186	2	08WU42	08wu42 homo sapien
12	257.5	22.9	268	2	06TN97	06tn97 homo sapien
13	257.5	22.9	273	2	09OXU3	09oxu3 rattus norv
14	204.5	18.2	66	2	06L866	06l866 rattus norv
15	175.5	15.6	203	2	08URF6	08urf6 brachydanio
16	168	14.9	248	1	MYPO_RAT	P06907 rattus norv
17	165	14.7	248	1	MYPO_MOUSE	P27573 mus musculu
18	164	14.6	248	1	MYPO_HUMAN	P25189 homo sapien
19	164	14.6	251	2	014902	014902 homo sapien
20	163.5	14.5	248	2	06WBR5	06wbr5 equus cabal
21	163	14.5	209	2	06DDH9	06ddh9 xenopus lae
22	162	14.4	219	1	MYPO_BOVIN	P10522 bos taurus
23	153	13.6	202	2	091406	091406 salmo sp. 1
24	152	13.5	235	2	06UWV2	06uwv2 mus sapien
25	151	13.4	215	2	06NW73	06nw73 brachydanio
26	150	13.3	215	1	EVAL_MOUSE	070255 mus musculu
27	150	13.3	215	2	091WI4	091wi4 mus musculu
28	147.5	13.1	215	1	EVAL_HUMAN	060487 homo sapien
29	145.5	12.9	246	1	MYPO_HETFR	P20938 heterodontu
30	142.5	12.7	229	2	08AVM3	08avm3 xenopus lae
31	136	12.1	249	1	MYPO_CHICK	P37301 gallus gall

32	132.5	11.8	270	2	06AYT8	06ayt8 rattus norv
33	131	11.6	243	2	09UEL4	09uel4 homo sapien
34	131	11.6	269	2	095297	095297 homo sapien
35	126.5	11.2	209	2	06GQX5	06gqx5 mus musculu
36	124.5	11.1	199	2	08UG36	08ug36 brachydanio
37	123	10.9	193	2	09UEL6	09uel6 homo sapien
38	123	10.9	209	2	09NYK4	09nyk4 homo sapien
39	121	10.8	202	2	08IX11	08ix11 homo sapien
40	120	10.7	233	2	08IX39	08ix39 homo sapien
41	115	10.2	222	2	08IX38	08ix38 homo sapien
42	115	10.2	287	2	09D7B8	09d7b8 mus musculu
43	113	10.0	215	1	CIB2_RAT	P54900 rattus norv
44	112	10.0	186	2	062861	062861 rattus norv
45	112	10.0	287	2	06SJP9	06sjp9 mus musculu

## ALIGNMENTS

RESULT 1  
CIB3\_RAT  
ID CIB3\_RAT STANDARD; PRT; 215 AA.  
AC 09jko0;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Sodium channel beta-3 subunit precursor.  
GN Name=Scn3b;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND PROBABLE DISULFIDE BONDS.  
RC TISSUE=Brain;  
RX MEDLINE=20160948; PubMed=10688874; DOI=10.1073/pnas.030362197;  
RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,  
RA Plincock R.D., Hughes J., Richardson P.J., Mizuguchi K., Jackson A.P.;  
RT "beta3: an additional auxiliary subunit of the voltage-sensitive  
RT sodium channel that modulates channel gating with distinct kinetics";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).  
RN [2]  
RP SEQUENCE FROM N.A., CHARACTERIZATION, TISSUE SPECIFICITY, AND SUBUNIT.  
RC STRAIN=Sprague-Dawley; TISSUE=Dorsal root ganglion;  
RX MEDLINE=21919106; PubMed=11922146; DOI=10.1006/mene.2001.1039;  
RA Qu Y., Curtis R., Lawson D., Gilbride K., Ge P., Distefano P.S.,  
RA Sliros-Santiago I., Catterall W.A., Scheuer T.;  
RT "Differential modulation of sodium channel gating and persistent  
RT sodium currents by the beta1, beta2, and beta3 subunits";  
RL Mol. Cell. Neurosci. 18:570-580(2001).  
RN [3]  
RP INTERACTION WITH NEUROFASCIN.  
RX MEDLINE=21363577; PubMed=11470829; DOI=10.1083/jcb.200102086;  
RA Redcliffe C.F., Westebroek R.E., Curtis R., Catterall W.A.;  
RT "Sodium channel beta1 and beta3 subunits associate with neurofascin  
RT through their extracellular immunoglobulin-like domain";  
RL J. Cell Biol. 154:427-434(2001).  
RN [4]  
RP FUNCTION: Modulates channel gating kinetics. Causes unique  
RP persistent sodium currents. Inactivates the sodium channel opening  
RP slower than the beta-1 subunit. Its association with neurofascin  
RP may target the sodium channels to the nodes of Ranvier of  
RP developing axons and retain these channels at the nodes in mature  
RP myelinated axons.  
RN [5]  
RP SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
RP conducting pore forming alpha-subunit regulated by one or more  
RP beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are  
RP noncovalently associated with alpha, while beta-2 is covalently  
RP linked by disulfide bonds. Beta-1 or beta-3 subunits associate  
RP with neurofascin.  
RN [6]  
RP SUBCELLULAR LOCATION: Type I membrane protein.  
RN [7]  
RP TISSUE SPECIFICITY: Expressed broadly in neurons in the central  
RN and peripheral nervous systems, but not in glia and most  
RN nonneuronal cells. Weak detection in lung and adrenal gland.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AJ243395; CAB76838.1; -  
DR EMBL: AF378093; AAK55415.1; -  
DR HSSP: P06907; INEU.  
DR InterPro: IPR007110; IG-1-like.  
DR Pfam: PF00047; 1g.1.  
DR PROSITE: PS50835; IG-LIKE; 1.  
KM Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;  
Signal; Sodium channel; Transmembrane; Voltage-gated channel.  
FT SIGNAL 1 24  
FT CHAIN 25 215  
FT DOMAIN 25 159  
FT TRANSMEM 160 180  
FT DOMAIN 181 215  
FT DOMAIN 25 138  
FT DISULFID 45 120  
FT CARBOHYD 95 95  
FT CARBOHYD 109 113  
FT CARBOHYD 113 121  
SQ SEQUENCE 215 AA; 24799 MW; 056B488E5EAEF4F CRC64;  
  
Query Match 100.0%; Score 1125; DB 1; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1e-94; Indels 0; Gaps 0;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MPAFRLPLASLVLIYWRVCPVCEVSETEAVOQNPMLRCISCKREVEATTVV 60  
DB 1 MPAFRLPLASLVLIYWRVCPVCEVSETEAVOQNPMLRCISCKREVEATTVV 60  
QY 61 EWFYRPGGKDFLIYRNGHOEVSPFGGRLOMNGSKDLOVSTIVLVNTLNDGGLTTC 120  
DB 61 EWFYRPGGKDFLIYRNGHOEVSPFGGRLOMNGSKDLOVSTIVLVNTLNDGGLTTC 120  
QY 121 NVSRFEFEARHPFKYTRRLIPLRVTEAGEDEFTSVSEIMMYILVFLTLMFTFEMTTC 180  
DB 121 NVSRFEFEARHPFKYTRRLIPLRVTEAGEDEFTSVSEIMMYILVFLTLMFTFEMTTC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215  
  
RESULT 2  
CIB3\_MOUSE STANDARD; PRT; 215 AA.  
AC Q8BHK2; O91299; Created)  
DT 29-MAR-2004 (Rel. 43; Last sequence update)  
DT 05-JUL-2004 (Rel. 44; Last annotation update)  
DE Sodium channel beta-3 subunit precursor.  
GN Name=Scn3b;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chen C., Avery C., Kazen-Gillespie K., Isom L.L.;  
RT "Mouse brain and heart beta 3 sodium channel cDNA."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBD databases.  
RN [2]  
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Head, and Spinal cord;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru T., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
RA Baldarilli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schimpl L.M., Knapman A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbali L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fough K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godik A., Gough J.,  
RA Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shmada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyse-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Atzawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
[3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, and Olfactory epithelium;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausberg R.V., Feingold E.A., Grouse L.H., Berge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Staleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.J.,  
RA Raha S.S., Loquejano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatirane P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,  
RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Nadeau A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -1- FUNCTION: Modulates channel gating kinetics. Causes unique  
CC persistent sodium currents. Inactivates the sodium channel opening  
CC slower than the beta-1 subunit. Its association with neurofascin  
CC may target the sodium channels to the nodes of Ranvier of  
CC developing axons (By similarity).  
CC myelinated axons (By similarity).  
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of one or  
CC conducting pore forming alpha-subunit regulated by one or more  
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are  
CC noncovalently associated with alpha, while beta-2 is covalently  
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate  
CC with neurofascin (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -----  
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CC EMBL: AY049036; AAL07512.1; -  
 CC EMBL: AK049747; BAC33901.1; -  
 CC EMBL: AK076466; BAC36356.1; -  
 CC EMBL: BC053919; AAH53919.1; -  
 CC EMBL: BC058636; AAH58636.1; -  
 CC HSSP: P06907; INEU.  
 CC MGI: MGI:1918882; Scn3b.  
 CC InterPro: IPR007110; Ig-like.  
 CC Pfam: PF00047; Ig\_1.  
 CC PROSITE: PS00835; IG-LIKE; 1.  
 CC Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;  
 CC Signal; Sodium channel; Transmembrane; Voltage-gated channel.  
 CC CHAIN 1 24 Potential.  
 CC DOMAIN 25 215 Sodium channel beta-3 subunit.  
 CC TRANSMEM 160 180 Extracellular (potential).  
 CC DOMAIN 181 215 Potential.  
 CC DISULFID 26 48 Cytoplasmic (potential).  
 CC FT 45 120 Ig-like C2-type.  
 CC CARBOHYD 95 95 Potential.  
 CC FT 109 109 N-linked (GlcNAc... ) (potential).  
 CC FT 113 113 N-linked (GlcNAc... ) (potential).  
 CC CARBOHYD 121 121 N-linked (GlcNAc... ) (potential).  
 CC SEQUENCE 215 AA; 24789 MW; 0E07B4704178A423 CRC64;

Query Match 99.3%; Score 1117; DB 1; Length 215;  
 Best Local Similarity 99.5%; Pred. No. 5.4e-94;  
 Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAFNLLPLASIVLIYWRVCPVCVEVPSSETEAVQGNPMKRCISCMKREBEVATTVV 60  
 DB 1 MPAFNLLPLASIVLIYWRVCPVCVEVPSSETEAVQGNPMKRCISCMKREBEVATTVV 60  
 QY 61 EWFYRPGGKDFLIYRNGHQEVESPFQGRLOMNGSKLDQVSIYLVNTLNDGSLYTC 120  
 DB 61 EWFYRPGGKDFLIYRNGHQEVESPFQGRLOMNGSKLDQVSIYLVNTLNDGSLYTC 120  
 QY 121 NVSRREFFEHARFPVKTTRILPLRVTEAGEDTSVSEIMYILVFLTMLFIEMITVC 180  
 DB 121 NVSRREFFEHARFPVKTTRILPLRVTEAGEDTSVSEIMYILVFLTMLFIEMITVC 180  
 QY 181 YRKVSKAEEMAOENASDYLAIPSENKENVVPVEE 215  
 DB 181 YRKVSKAEEMAOENASDYLAIPSENKENVVPVEE 215

RESULT 3  
 ID 069203 PRELIMINARY; PRT; 268 AA.  
 AC 069203;  
 DT 25-OCT-2004 (TEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)  
 DE MKIAA1158 protein (Fragment).  
 GN Name=MKIAA1158;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraka S.,  
 RA Suga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,  
 RA Nagase T., Ohara O., Koga H.;  
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:  
 RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous  
 RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones

RT Randomly Sampled from Sike-Fractionated Libraries.;

RU DNA Res. 11:205-218(2004).  
 DR EMBL: AK173115; BAD3293.1; -  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00409; Ig\_1.  
 DR SMART: SM00406; Ig\_1.  
 DR PROSITE: PS00835; IG-LIKE; 1.  
 DR NON TER 1  
 SQ SEQUENCE 268 AA; 30330 MW; 7A265D5DD2409F CRC64;

Query Match 99.3%; Score 1117; DB 2; Length 268;  
 Best Local Similarity 99.5%; Pred. No. 6.9e-94;  
 Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAFNLLPLASIVLIYWRVCPVCVEVPSSETEAVQGNPMKRCISCMKREBEVATTVV 60  
 DB 54 MPAFNLLPLASIVLIYWRVCPVCVEVPSSETEAVQGNPMKRCISCMKREBEVATTVV 113  
 QY 61 EWFYRPGGKDFLIYRNGHQEVESPFQGRLOMNGSKLDQVSIYLVNTLNDGSLYTC 120  
 DB 114 EWFYRPGGKDFLIYRNGHQEVESPFQGRLOMNGSKLDQVSIYLVNTLNDGSLYTC 173  
 QY 121 NVSRREFFEHARFPVKTTRILPLRVTEAGEDTSVSEIMYILVFLTMLFIEMITVC 180  
 DB 174 NVSRREFFEHARFPVKTTRILPLRVTEAGEDTSVSEIMYILVFLTMLFIEMITVC 233  
 QY 181 YRKVSKAEEMAOENASDYLAIPSENKENVVPVEE 215  
 DB 234 YRKVSKAEEMAOENASDYLAIPSENKENVVPVEE 268

RESULT 4  
 ID CIB3 HUMAN STANDARD; PRT; 215 AA.  
 AC G9NY72; O9UR2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Sodium channel beta-3 subunit precursor.  
 GN Name=SCN3B; Synonyms=KIAA1158;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20160948; PubMed=10688874; DOI=10.1073/pnas.030362197;  
 RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,  
 RA Plimack R.D., Higgs J., Richardson P.J., Mizuguchi K., Jackson A.P.;  
 RT "Beta3: an additional auxiliary subunit of the voltage-sensitive  
 RT sodium channel that modulates channel gating with distinct kinetics.;"  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).  
 RU [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mygdala;  
 RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;  
 RA Wiemann S., Weil B., Wellenreuther R., Gaassenhuber J., Glassl S.,  
 RA Ansoorge W., Boecher M., Bloeker H., Baetsachs S., Blum H.,  
 RA Lauber U., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,  
 RA Newes H.-W., Oetjenwaelder B., Obermaier B., Tampe J., Heubner D.,  
 RA Wamboldt R., Korn B., Pousetka A.;  
 RT "Towards a catalog of human genes and proteins: sequencing and  
 RT analysis of 500 novel complete protein coding human cDNAs.;"  
 RT Genome Res. 11:422-435(2001).  
 RU [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20039618; PubMed=10574461;  
 RA Hirose M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,

Query Match	98.2%	Score 1105	DB 1	Length 215
Best Local Similarity	98.1%	Pred. No. 6	8e-93	
Matches 211	Conservative	0	Mismatches 4	Indels 0
			Gaps	0
1	MPAFRLRLPLASLIVLIVWVRCVPCVBPSTEAQVQNPMLKRLRISCMKREVEATVIV	60		
Db	1	MPAFRLRLPLASLIVLIVWVRCVPCVBPSTEAQVQNPMLKRLRISCMKREVEATVIV	60	
Qy	61	EMFYRPEGKDFLIEYRNGHOEVSPPQGRLOMNGSKDLDVSTIVNTNLINDSGLYTC	120	
Db	61	EMFYRPEGKDFLIEYRNGHOEVSPPQGRLOMNGSKDLDVSTIVNTNLINDSGLYTC	120	
Qy	121	NVSRBFEEFARHPFVKTRRLPLRVTBEGEDFTSVSEIMWYILVFLTLMLFIEMLYC	180	
Db	121	NVSRBFEEFARHPFVKTRRLPLRVTBEGEDFTSVSEIMWYILVFLTLMLFIEMLYC	180	
Qy	181	YRKVSKAEBAQENASDYALIPSENKENSIVPVVEE	215	

DB	181	YRKYSKAEAAQENASDYLAIPESENKNSAPVBE	215
RESULT 5			
CIB3_MACFA			
ID_CIB3_MACFA	STANDARD;	PRT;	215 AA.
AC	08HXJ7;		
DT	29-MAR-2004 (Rel. 43, Created)		
DT	29-MAR-2004 (Rel. 43, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Sodium channel beta-3 subunit precursor (Qmoa-13657) .		
OS	Name=SCN3B;		
OC	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey) .		
OC	Eukaryota; Metazoa; Chordata; Crniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;		
OX	Cercopitheciinae; Macaca.		
NCBI_TaxID=9541;			
RV	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Medulla oblongata;		
RA	Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;		
RL	Submitted (DDBJ-2002) to the EMBL/GenBank/DBJ databases.		
CC	-I- FUNCTION: Modulates channel gating kinetics. Causes unique		
CC	persistent sodium currents. Inactivates the sodium channel opening		
CC	slower than the beta-1 subunit. Its association with neurofascin		
CC	may target the sodium channels to the nodes of Ranvier of		
CC	myelinated axons (By similarity) .		
CC	-I- SUBUNIT: The voltage-sensitive sodium channel consists of an ion		
CC	conducting pore forming alpha-subunit regulated by one or more		
CC	beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are		
CC	noncovalently associated with alpha. While beta-2 is covalently		
CC	linked by disulfide bonds. Beta-1 or beta-3 subunits associate		
CC	with neurofascin (By similarity) .		
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity) .		
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.		
CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -		
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CC	or send an email to <a href="mailto:license@isb.ch">license@isb.ch</a> ).		
CC			
DR	EMBL; AB097521; BAC41746.1; -		
DR	HSPB; P06907; INEU.		
DR	InterPro: IPR007110; Ig-like.		
DR	Pfam; PF00047; Ig_1.		
DR	PROSITE; PS50833; Ig_LIKE; 1.		
KW	Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;		
KW	Signal; Sodium channel; Transmembrane; Voltage-gated channel.		
FT	SIGNAL	1	22
FT	CHAIN	23	215
FT	DOMAIN	23	159
FT	TRANSSEM	160	180
FT	DOMAIN	181	215
FT	DOMAIN	24	138
FT	DISULFID	26	48
FT	DISULFID	45	120
FT	CARBOHYD	95	95
FT	CARBOHYD	109	109
FT	CARBOHYD	113	113
FT	CARBOHYD	121	121
SEQUENCE	215 AA; 24702 MW; 25313D5ED218AACF CRC64;		
Query Match	97.5%; Score 10971; DB 1; Length 215;		
Best Local Similarity	97.2%; Pred. No. 3.6e-92;		
Matches 209; Conservative	0; Mismatches 6; Indels 0; Gaps 0;		
1	MPANRLPLASVLTITWVGVCFVCEVSESTAVNCGNPMKLRICICGMKREEVATTVV	60	

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Db      1 MPAFNRLPLASVILVLYWVCPVCEVPSEREAQVGNPMKLRGICSMKREBEVATTVV 60
Qy      61 EMFYRPEGKDFLIYERNGHOEVESPFOGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120
Db      61 EMFYRPEGKDFLIYERNGHOEVESPFOGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120
Qy      121 NVSRFEFEHARFPVKTRILPLRVTEBAGEDFTSVSEIMYTLVFLTMLFIEMITVC 180
Db      121 NVSRFEFEHARFPVKTRILPLRVTEBAGEDFTSVSEIMYTLVFLTMLFIEMITVC 180
Qy      181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215
Db      181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 6
Q6DB47  PRELIMINARY; PRT; 215 AA.
AC      06DE47;
DT      25-OCT-2004 (TEMBLrel. 28, Created)
DT      25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE      Scn3b-p1ov protein.
GN      Name=scn3b-p1ov;
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC      Xenopodidae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Krausberg R.L., Feingold E.A., Grouse L.H., Shemen C.M., Schuler G.D.,
RA      Krausberg R.L., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.D., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Lottmann N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA      Krzyvinksi M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Maier M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Klein S., Gerhard D.S.;
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DB      EMBL: BC077295; AAH77295.1; -
DR      InterPro: IPR003599; IG_
DR      InterPro: IPR007110; IG-like.
DR      InterPro: IPR003596; IG_v.
DR      SMART; SM00409; IG; 1.
DR      SMART; SM00406; IG; 1.

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DR      PROSITE; PS50835; IG LIKE; 1.
SQ      SEQUENCE 215 AA; 24472 MW; 2AAB890E46DE0289 CRC64;
Query Match 62.2%; Score 700; DB 2; Length 215;
Best Local Similarity 61.9%; Pred. No. 7, 4e-56;
Matches 133; Conservative 31; Mismatches 51; Indels 0; Gaps 0;

Qy      1 MPAFNRLPLASVILVLYWVCPVCEVPSEREAQVGNPMKLRGICSMKREBEVATTVV 60
Db      1 MAAMENIFWTDSTVLLFLMVVFCSPVCEVOSGTEAKGEMTLICSMKREBEVATTNV 60
Qy      61 EMFYRPEGKDFLIYERNGHOEVESPFOGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120
Db      61 RMFYQPEDGDELIVFEDGKPLDKSPLOGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120
Qy      121 NVSRFEFEHARFPVKTRILPLRVTEBAGEDFTSVSEIMYTLVFLTMLFIEMITVC 180
Db      121 HVNRTHLFDHHRSTOSKSLTKVMEBAGEDFTSVSKIMMYTLAFLTFMLLVEAYC 180
Qy      181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215
Db      181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 7
CIB1_RABBIT STANDARD; PRT; 218 AA.
AC      P53788;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Sodium channel beta-1 subunit precursor.
GN      Name=SCN1B;
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=New Zealand white; TISSUE=Sciatic nerve;
RX      MEDLINE=96235151; PubMed=8666261; DOI=10.1016/0378-1119(95)00871-3;
RA      Belcher S.M., Howe J.R.;
RT      "Cloning of the cDNA encoding the sodium channel beta 1 subunit from
RT      rabbit";
RL      Gene 170:285-286(1996).
RN      [1]
RP      FUNCTION: Crucial in the assembly, expression, and functional
RP      modulation of the heterotrimeric complex of the sodium channel.
RP      The beta-1 subunit can modulate multiple alpha subunit isoforms
RP      from brain, skeletal muscle, and heart. Its association with
RP      neurofascin may target the sodium channels to the nodes of Ranvier
RP      of developing axons and retain these channels at the nodes in
RP      mature myelinated axons (By similarity).
RN      [1]
RP      SUBUNIT: The voltage-sensitive sodium channel consists of an ion
RP      conducting pore forming alpha-subunit regulated by one or more
RP      beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
RP      associated with alpha, while beta-2 is covalently linked by
RP      disulfide bonds. Beta-1 or beta-3 subunits associate with
RP      neurofascin (By similarity).
RN      [1]
RP      SUBCELLULAR LOCATION: Type I membrane protein.
RN      [1]
RP      SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
RN      [1]
RP      This SWISS-PROT entry is copyright. It is produced through a collaboration
RP      between the Swiss Institute of Bioinformatics and the EMBL outstation -
RP      the European Bioinformatics Institute. There are no restrictions on its
RP      use by non-profit institutions as long as its content is in no way
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RP      entities requires a license agreement (See http://www.isb-sib.ch/announce/
RP      or send an email to license@isb-sib.ch).
RN      [1]
DB      EMBL; U35382; AAB17572.1; -
DR      PIR; JC4788; JC4788.
DR      InterPro: IPR007110; IG-like.
DR      Pfam; PF00047; IG; 1.

```

DR PROSITE; PS50835; IG-LIKE; FALSE NEG.  
 KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;  
 KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.  
 FT SIGNAL 1 18 By similarity.  
 FT CHAIN 19 218 Sodium channel beta-1 subunit.  
 FT DOMAIN 19 160 Extracellular (Potential).  
 FT TRANSMEM 161 182 Potential.  
 FT DOMAIN 183 218 Cytoplasmic (Potential).  
 FT DOMAIN 22 150 Ig-like C2-type.  
 FT DISULFID 21 43 Potential.  
 FT DISULFID 40 121 Potential.  
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 218 AA, 24706 MW, 39BD174E1FAE7FD2 CRC64;  
 Query Match 41.8%; Score 470.5; DB 1; Length 218;  
 Best Local Similarity 49.3%; Pred. No. 7.3e-35;  
 Matches 105; Conservative 29; Mismatches 64; Indels 15; Gaps 6;  
 QY 6 RLPL-ASVLYIVWVRCFVCEVSETEAVGQGNPKKLCISCKRKEEATTVEM 62  
 DB 3 RLALVVGALVSSAM-----GCVEVDSVETAVGMTFKILCISCKRSETTATFTBW 57  
 QY 63 FYRPGGKDFL-IVEYRNGHQEVESP--FOGRLQWNGS---KDLQVSTITVLTNLSG 116  
 DB 58 TFRQGTSEFEVKILTYENEVLDLEDEREGRVWVNGSGTDLQDLSTFINVTVYNSG 117  
 QY 117 LYTGVNSFEFEHARPPVKTTRLIPRYTEBAGDFSVSEIMYIIVLTLMPLF 176  
 DB 118 DVQCHVYRLSPENYEHTNSVVKIHLVVDKANDMDMSIVSEIMYIIVLTLMVAE 177  
 QY 177 MYCYRKVSKA-EBAAGVNASDYLAIPSENKEN 208  
 DB 178 MYCYKIAATEAAAGVNASDYLAIPSENKEN 210  
 Db  
 RESULT 8  
 CIB1\_HUMAN STANDARD; PRT; 218 AA.  
 AC 007699;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Sodium channel beta-1 subunit precursor.  
 GN Name=SCN1B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RC MEDLINE=93357746; PubMed=8394762;  
 RA McCatchey A.L., Cannon S.C., Slaugenhaupt S.A., Guseella J.F.;  
 RT "The cloning and expression of a sodium channel beta 1-subunit cDNA  
 from human brain.";  
 RL Hum. Mol. Genet. 2:745-749(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart, and Skeletal muscle;  
 RC MEDLINE=94171787; PubMed=8125980;  
 RA Makita N., Bennett P.B. Jr., George A.L. Jr.;  
 RT "Voltage-gated Na+ channel beta 1 subunit mRNA expressed in adult  
 human skeletal muscle, heart, and brain is encoded by a single gene.";  
 RL J. Biol. Chem. 269:7571-7578(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RC MEDLINE=95154833; PubMed=7851891;  
 RA Makita N., Sloan-Brown K., Wegnits D.O., Ropers H.-H.,  
 RA George A.L. Jr.;

RT "Genomic organization and chromosomal assignment of the human voltage-  
 gated Na+ channel beta 1 subunit gene (SCN1B).";  
 RL Genomics 23:628-634(1994).  
 RN [4]  
 RP VARIANT GFS+ TRP-121.  
 RX MEDLINE=96361163; PubMed=9697698; DOI=10.1038/1252;  
 RA Wallace R.H., Wang D.W., Singh R., Scheffer I.E., George A.L. Jr.,  
 RA Phillips H.A., Saar K., Reis A., Johnson E.W., Sutherland G.R.,  
 RA Berkovic S.F., Mulley J.C.;  
 RT "Febrile seizures and generalized epilepsy associated with a mutation  
 in the Na(+) channel beta-1 subunit gene SCN1B.";  
 RL Nat. Genet. 19:366-370(1998).  
 CC -1- FUNCTION: Crucial in the assembly, expression, and functional  
 modulation of the heterotrimeric complex of the sodium channel.  
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms  
 from brain, skeletal muscle, and heart. Its association with  
 neurofascin may target the sodium channels to the nodes of Ranvier  
 or developing axons and retain these channels at the nodes in  
 mature myelinated axons.  
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
 conducting pore forming alpha-subunit regulated by one or more  
 beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently  
 associated with alpha, while beta-2 is covalently linked by  
 disulfide bonds. Beta-1 or beta-3 subunits associate with  
 neurofascin.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, heart  
 and brain.  
 CC -1- DISEASE: Defects in SCN1B are a cause of generalized epilepsy with  
 febrile seizures plus (GFS+) [MIM:604233]. GFS+ is a disease  
 characterized by a highly variable phenotype combining febrile  
 seizures, generalized seizures often precipitated by fever at age  
 6 years or more, and partial seizures, with a variable degree of  
 severity.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
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 CC  
 DR EMBL, L10338; AAA60391.1; -;  
 DR EMBL, L16242; AAA61277.1; -;  
 DR EMBL, U12193; AAB97608.1; -;  
 DR EMBL, U12189; AAB97608.1; JOINED.  
 DR EMBL, U12190; AAB97608.1; JOINED.  
 DR EMBL, U12191; AAB97608.1; JOINED.  
 DR EMBL, U12192; AAB97608.1; JOINED.  
 DR PIR, A55734; A55734.  
 DR GeneW, HGNC:10586; SCN1B.  
 DR MIM, 600235; -;  
 DR MIM, 604233; -;  
 DR GO, GO:0005248; F: voltage-gated sodium channel activity; TAS.  
 DR GO, GO:0006814; P: sodium ion transport; TAS.  
 DR GO, GO:0007268; P: synaptic transmission; TAS.  
 DR InterPro, IPR007110; Ig-like.  
 DR Pfam, PF00447; Ig-1.  
 DR PROSITE, PS50835; IG-LIKE; FALSE NEG.  
 KW Disease mutation; Epilepsy; Glycoprotein; Immunoglobulin domain;  
 KW Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane;  
 KW Voltage-gated channel.  
 FT SIGNAL 1 18 Potential.  
 FT CHAIN 19 218 Sodium channel beta-1 subunit.  
 FT DOMAIN 19 160 Extracellular (Potential).  
 FT TRANSMEM 161 182 Potential.  
 FT DOMAIN 183 218 Cytoplasmic (Potential).  
 FT DOMAIN 22 150 Ig-like C2-type.  
 FT DISULFID 21 43 Potential.  
 FT DISULFID 40 121 Potential.  
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).  
 FT

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FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
FT VARIANT 121 121 C->W (in GERS+).
SQ SEQUENCE 218 AA; 24707 MW; 09B812FA3F9E9018 CRC64;
Query Match 41.5%; Score 466.5; DB 1; Length 218;
Best Local Similarity 51.6%; Pred. No. 1.7e-34;
Matches 99; Conservative 26; Mismatches 57; Indels 7; Gaps 4;
QY 26 CVEVPSTEAIVQGNPKLRICSCMKREVEATVVEVFRPEGKDFL-ITYENRNGHOEV 84
DB 21 CVEVDSETEAVVGMFTFKILICISCKRSETTAETFTETFPQKTEEFVKILRYENEVLQL 80
QY 85 ESP--FQGRLOWNGS---KDLQDVSTIVANTLNDGSLTYCNVSRPEFEAHRRPFTKTR 139
DB 81 EEDEREFGRRVWVMSRGTDLPDLSIFITVTVNHSQDYCHYVRLFFPNYEHNSTSVK 140
QY 140 LIPLRVTEAGEDEFTSVSEIMMYILVFLTLFEMICYRVKSKA-BEAAQENASDY 198
DB 141 KIHLEVDKRNDRMASIVSEIMYIVLVITLVLAEMICYKKAAPATAAQNASEY 200
QY 199 LAIPSENKEN 208
DB 201 LAITSESKEN 210
RESULT 9
CIB1_RAT STANDARD; PRT; 218 AA.
ID CIB1_RAT
AC 000954;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel beta-1 subunit precursor.
GN Name=Scn1b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92271207; PubMed=1375395.
RA Isom L.V., De Jongh K.S., Patton D.E., Reber B.F.X., Offord J.,
RA Charbonneau H., Walsh K., Goldin A.L., Catterall W.A.;
RT "Primary structure and functional expression of the beta 1 subunit of
RT the rat brain sodium channel.";
RL Science 256:839-842 (1992).
RN 12
RP INTERACTION WITH NEUROFASCIN.
RX MEDLINE=21363577; PubMed=11470829; DOI=10.1083/jcb.200102086;
RA Ratcliffe C.F., Westbroek R.E., Curtis R., Catterall W.A.;
RT "Sodium channel beta1 and beta3 subunits associate with neurofascin
RT through their extracellular immunoglobulin-like domain.";
RL J. Cell Biol. 154:427-434 (2001).
CC -1- FUNCTION: Crucial in the assembly, expression, and functional
CC modulation of the heterotrimeric complex of the sodium channel.
CC The beta-1 subunit can modulate multiple alpha subunit isoforms
CC from brain, skeletal muscle, and heart. Its association with
CC neurofascin may target the sodium channels to the nodes of Ranvier
CC of developing axons and retain these channels at the nodes in
CC mature myelinated axons.
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
CC conducting pore forming alpha-subunit regulated by one or more
CC beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
CC associated with alpha, while beta-2 is covalently linked by
CC disulfide bonds. Beta-1 or beta-3 subunits associate with
CC neurofascin.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, heart, skeletal muscle and
CC spinal cord.

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CC -1- DEVELOPMENTAL STAGE: In developing nodes of Ranvier, it is
CC localized in the sciatic nerve at postnatal days 3 and 10, during
CC the process of myelination and maturation of the nodes.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC
CC * THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M91808; AAA88513.1; -.
DR PIR: A42737; A42737.
DR RGD: 3631; Scn1b.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig_1.
DR PROSITE: PS50835; IG LIKE; FALSE NEG.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane;
KW Voltage-gated channel.
FT SIGNAL 1 18
FT CHAIN 19 218 Sodium channel beta-1 subunit.
FT DOMAIN 19 160 Extracellular (Potential).
FT TRANSMEM 161 182 Potential.
FT DOMAIN 183 218 Cytoplasmic (Potential).
FT DOMAIN 22 150 Ig-like C2-type.
FT DISULFID 21 43 Potential.
FT DISULFID 40 121 Potential.
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 218 AA; 24692 MW; 0BA84FC44FE2306B CRC64;
Query Match 41.2%; Score 463.5; DB 1; Length 218;
Best Local Similarity 51.1%; Pred. No. 3.2e-34;
Matches 97; Conservative 29; Mismatches 57; Indels 7; Gaps 4;
QY 26 CVEVPSTEAIVQGNPKLRICSCMKREVEATVVEVFRPEGKDFL-ITYENRNGHOEV 84
DB 21 CVEVDSETEAVVGMFTFKILICISCKRSETTAETFTETFPQKTEEFVKILRYENEVLQL 80
QY 85 ESP--FQGRLOWNGS---KDLQDVSTIVANTLNDGSLTYCNVSRPEFEAHRRPFTKTR 139
DB 81 EEDEREFGRRVWVMSRGTDLPDLSIFITVTVNHSQDYCHYVRLFFPNYEHNSTSVK 140
QY 140 LIPLRVTEAGEDEFTSVSEIMMYILVFLTLFEMICYRVKSKA-BEAAQENASDY 198
DB 141 KIHLEVDKRNDRMASIVSEIMYIVLVITLVLAEMICYKKAAPATAAQNASEY 200
QY 199 LAIPSENKEN 208
DB 201 LAITSESKEN 210
RESULT 10
CIB1_MOUSE STANDARD; PRT; 218 AA.
ID CIB1_MOUSE
AC P97952;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel beta-1 subunit precursor.
GN Name=Scn1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;

```



RX MEDLINE=97165884; PubMed=9013777; DOI=10.1016/S0169-328X(96)00123-4;  
 RA Grosson C.L.S., Cannon S.C., Corey D.P., Gussella J.F.;  
 RT "Sequence of the voltage-gated sodium channel beta1-subunit in wild-  
 RT type and in quivering mice.";  
 RL Brain Res. Mol. Brain Res. 42:222-226(1996).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98387156; PubMed=9721701;  
 RA Kuperlshmidt S., Yang T., Roden D.M.;  
 RT "Modulation of cardiac Na<sup>+</sup> current phenotype by beta1-subunit  
 RT expression.";  
 RL Circ. Res. 83:441-447(1998).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.T., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Crucial in the assembly, expression, and functional  
 CC modulation of the heterotrimeric complex of the sodium channel.  
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms  
 CC from brain, skeletal muscle, and heart. Its association with  
 CC neurofascin may target the sodium channels at the nodes of Ranvier  
 CC of developing axons and retain these channels at the nodes in  
 CC mature myelinated axons (By similarity).  
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
 CC conducting pore forming alpha-subunit regulated by one or more  
 CC beta-1, beta-2 and beta-3. Beta-1 and beta-2 are noncovalently  
 CC associated with alpha, while beta-3 is covalently linked by  
 CC disulfide bonds. Beta-1 or beta-3 subunits associate with  
 CC neurofascin (By similarity).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U46681; AAC53006.1; -;  
 DR EMBL: U85786; AAB49368.1; -;  
 DR EMBL: BC009652; AAH09652.1; -;  
 DR EMBL: BC039140; AAH39140.1; -;  
 DR MGD: MGI:98247; Scln1b.  
 DR InterPro: IPR007110; I9-1like.  
 DR Pfam: PF00047; 1g\_1.  
 DR PROSITE: PS50835; 1G\_LIKE; FALSE NEG.  
 KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;  
 KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.  
 FT SIGNAL 1 18 By similarity.  
 FT CHAIN 19 218 Sodium channel beta-1 subunit.  
 FT DOMAIN 19 160 Extracellular (Potential).

FT TRANSMEM 161 182 Potential.  
 FT DOMAIN 183 218 Cytoplasmic (Potential).  
 FT FT 22 150 Ig-like C2-type.  
 FT DISULFID 21 43 Potential.  
 FT DISULFID 40 121 Potential.  
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 218 AA; 24650 MW; 5198F383B0A8C65 C6C64;  
 Query Match 41.0%; Score 461, DB 1; Length 218;  
 Best Local Similarity 48.8%; Pred. No. 5,4e-34;  
 Matches 100; Conservative 31; Mismatches 62; Indels 12; Gaps 5;  
 QY 11 ASVLIVYVVRCPFCVPEPSETFAVQGNPMKLCISGMKREVEATVVFMPRECGK 70  
 DB 11 AALVSSAW-----GGCVVDSDTEAVGMTRKILCISCKRSETTAETFTWTRQKTE 65  
 QY 71 DFL-IYERYNGHOEVESESP--FQGRLOWNGS--XDLQDVSTIVLVTLNDSGLYTCVNSR 124  
 DB 66 EFVKIRKRENEVLQLEDEDEREGRVVWNGSGRTDLDLSIFITNVTVNHSGDYECCHYR 125  
 QY 125 EEFEPARPPVKYTRLLPLRVTEBAGDEFTSVSGIMMYIILVPLTLMFTMTYCRKV 184  
 DB 126 LLFEDNYEHTNSVVKIHLLEVVDKRNDRMASIVSEIMMYVILVILTVLVAEMVYCYKXI 185  
 QY 185 SKA--EAAQENASDYLAIPISENKEN 208  
 DB 186 AATFAAQAQENASEYLAITTSSEKEN 210  
 RESULT 11  
 Q8WU42 PRELIMINARY; PRT; 186 AA.  
 AC Q8WU42;  
 DT 01-MAR-2002 (TRENBLREL. 20, Created)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
 DE SCN1B protein (Fragment).  
 GN Name=SCN1B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.T., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;





Job time : 118 secs

RX MEDLINE=95024086; PubMed=7937931;  
RA Oh Y., Waxman S.G.;  
RT "The beta 1 subunit mRNA of the rat brain Na+ channel is expressed in  
RT glial cells";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:9985-9989(1994).  
DR EMBL; L48688; AAB02428.1; -;  
DR GO; GO:0005216; F:ion channel activity; IEA.  
KW Ionic channel.  
FT NON TER  
SQ SEQUENCE 66 AA; 7208 MW; 4DB598740914D95B CRC64;

Query Match 18.2%; Score 204.5; DB 2; Length 66;  
Best Local Similarity 67.2%; Pred. No. 4e-11;  
Matches 39; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 152 DFTSVSEIMMYILVFLTWLFIEMICYRVSKA-EAAQENASDYLAIPSENKEN 208  
DB 1 DWASTVSEIMMYILVFLTWLVAEMVICYKKAATAEAAQENASEYLAITSSEKEN 58

## RESULT 15

Q8JFG6 PRELIMINARY; PRT; 203 AA.  
AC Q8JFG6;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Myelin protein zero.  
GN Name=mpz;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Myelin;  
RA Schweitzer J., Becker T., Becker C.G., Schachner M.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ489219; CAD32961.1; -;  
DR HSSP; P06907; INEU.  
DR ZFIN; ZDB-GENE-010724-4; mpz.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR009320; Myelin\_PO.  
DR PRINTS; PRO0213; MYELINPO.  
DR SMART; SM00409; IG\_1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
SQ SEQUENCE 203 AA; 22097 MW; 12614E9076D373D1 CRC64;

Query Match 15.6%; Score 175.5; DB 2; Length 203;

Best Local Similarity 26.5%; Pred. No. 6.4e-08;  
Matches 53; Conservative 41; Mismatches 89; Indels 17; Gaps 7;

QY 7 LPLPLSLVLIYVWRCFPCVCEVPSETEAVQGNPKLRICISCMKREVEATTVEMFYRP 66  
DB 4 VLALTSVVLIGLIGSSTLAVVTDSSEKALVGSVRLSC-SFSSNQWTSPEVSPFTWHYRP 62  
QY 67 EGGRKDFL-IYERYNG--HOEVESPPQGRLOMNGSKDLODVSTIVNTLNDGLTCNVIS 123  
DB 63 DGAKDAISIFHYGGGEAVPANKPQNRLFEVGNPSRDSILIKNLDGDNGTFTCDAK 122  
QY 124 REFEEFARHPFKTRRLIPL-RVTEAGEDFTSVSEIMMYILV----FLTWLFIEMI 178  
DB 123 NPPDIGH--PSTRRLVFERKVPVQAGVTGSTITGVGLILVVAIYILMRFLVARRV 179  
QY 179 YC-----YRKVSKAEAAQE 193  
DB 180 FSLSMKHKGKGKKGEGSQ 199

Search completed: March 31, 2005, 20:21:49

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## OM protein - protein search, using sw model

Run on: March 31, 2005, 20:01:32 ; Search time 124.5 Seconds  
(without alignments)  
667.899 Million cell updates/sec

Title: US-09-977-579-2

Perfect score: 1124  
Sequence: 1 MPANRFLPLASLVLYWVS.....SDYLAIPESENKSAVPEE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124	100.0	215	3	AAB36002 Human bet
2	1124	100.0	215	4	AAB85206 Human nov
3	1124	100.0	215	5	ABB05689 Human sig
4	1124	100.0	215	6	Aae35366 Human sod
5	1124	100.0	215	7	ABR83183 Human SCN
6	1105	98.3	215	3	AAB36001 Rat betas
7	1105	98.3	215	4	AAB50243 Rat betas
8	1105	98.3	215	6	AAB35367 Rat sodiu
9	1024	91.1	195	4	AAW79212 Human pro
10	986	87.7	191	4	AAB50245 Rat sodiu
11	942.5	83.9	369	4	ABG2577 Novel hum
12	843	75.0	159	3	AAB36020 Human bet
13	834	74.2	157	8	ADSI0835 Human the
14	832	74.0	159	3	AAB36021 Rat betas
15	694	61.7	1176	4	ABG22576 Novel hum
16	477	42.4	218	4	AAB50260 Rabbit so
17	472	42.0	218	3	AAB36031 Rat betai
18	472	42.0	218	4	AAB62326 Rat sodiu
19	471	41.9	218	6	ABB82771 Human vol
20	471	41.9	218	7	AAB35363 Human sod
21	471	41.9	218	8	ABR83181 Human SCN
22	471	41.9	218	8	ADM67223 Human vol
23	471	41.8	218	8	ADQ19429 Human sof
24	470	41.8	218	7	ADB78601 Human sod
25	463	41.2	218	7	ADB78602 Human sod

26	408.5	36.3	206	4	ABG22575 Novel hum
27	258.5	23.0	268	5	AAB18634 Human bet
28	246	21.9	272	4	AAB62320 Rat sodiu
29	246	21.9	272	4	AAB20371 Sodium ch
30	234	20.8	74	4	ABBI1698 Human vol
31	234	20.8	74	4	AAAB0196 Human pro
32	207	18.4	39	3	AAB36015 Human bet
33	196	17.4	39	3	AAB36016 Rat betas
34	175	15.6	248	7	ADSE6862 Rat prote
35	167	14.9	248	6	ABM04838 Rat scitwa
36	165	14.7	34	3	AAB36029 Human bet
37	163.5	14.5	258	5	AAAM52696 Human mye
38	161	14.3	34	3	AAB36034 Rat betas
39	160.5	14.3	235	4	AAV72879 Human PRO
40	160.5	14.3	235	4	AAU83710 Human tra
41	160.5	14.3	235	5	AAU83710 Human PRO
42	160.5	14.3	235	6	ABU80857 Human PRO
43	160.5	14.3	235	6	ABO33823 Novel hum
44	160.5	14.3	235	6	ABG74763 Human PRO
45	160.5	14.3	235	6	ABU82166 Novel hum

## ALIGNMENTS

RESULT 1  
ID AAB36002 standard; protein; 215 AA.

AC AAB36002;

DT 15-FEB-2001 (first entry)

DE Human betas3 subunit.

XX Human, beta sub-unit; betas3; analgesic; anticonvulsant;

KW cerebroprotective; vasotropic; cardiant; nootropic; cytostatic;

KW dermatological; gene therapy; voltage-gated sodium channel; pain;

KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;

KW familial nonchromatin paraganglioma; phenylketonuria;

KW Charcot Marie Tooth disease.

XX Homo sapiens.

XX W0200063367-A1.

PD 26-OCT-2000.

XX 24-FEB-2000; 2000WO-EP001783.

PF 15-APR-1999; 99US-0129473P.

PR (WARN) WARNER LAMBERT CO.

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI Cox P, Dixon A, Jackson A, Morgan K;

XX WPI; 2000-665241/64.

XX N-PSDB; AAC67837.

DR Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium

PT channel, and their corresponding polypeptides, useful for detecting and

PT treating sodium channel-associated conditions, e.g. pain, epilepsy and

PT stroke.

XX Claim 34; Fig 4; 88pp; English.

XX The present sequence is given in the claims of a specification relating

CC to a novel family of beta sub-unit proteins from a voltage-gated sodium

CC channel. Human and rat beta sub-units, which have been collectively

CC identified as betas3, have been isolated. The polynucleotides and

CC polypeptides are useful for screening for agonists and antagonists of

CC sodium channels. The agonists, antagonists, proteins and nucleic acids

CC may be used diagnosing of treating diseases or conditions associated with  
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,  
CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,  
CC Phenylketonuria and Charcot Marie Tooth disease  
XX

XX Sequence 215 AA;

Query Match . . . 100.0%; Score 1124; DB 3; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2,4e-98;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYVWSVCFPVCEVPSSETEAQGNPKMRLRCISCKKREVEATTIV 60  
DB 1 MPAFNRLLPLASLVLIYVWSVCFPVCEVPSSETEAQGNPKMRLRCISCKKREVEATTIV 60  
QY 61 EMFYRPEGKDFLIYEYRNGHOEVSPFOGRLQWNGSKDLDVSTIVNTLNDGGLTTC 120  
DB 61 EMFYRPEGKDFLIYEYRNGHOEVSPFOGRLQWNGSKDLDVSTIVNTLNDGGLTTC 120  
QY 121 NVSRREFEFAHRPFVKTRRLIPLRVTEBAGEDFTSVSEIMMYILLVFLTMLLLEMTYC 180  
DB 121 NVSRREFEFAHRPFVKTRRLIPLRVTEBAGEDFTSVSEIMMYILLVFLTMLLLEMTYC 180  
QY 181 YRKVSKAEBAQAQENASDYLAIPSENKENSAPVVEE 215  
DB 181 YRKVSKAEBAQAQENASDYLAIPSENKENSAPVVEE 215

RESULT 2

ABB85206  
ID AAB85206 standard; protein; 215 AA.

XX AAB85206;

XX 07-SEP-2001 (first entry)

DE Human novel sodium channel betal-like subunit.

XX Sodium channel; sensory neurone specific channel; betal-like subunit;

KW SNS; therapeutic; pain; analgesic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 38..122 /note="immunoglobulin domain"

FT Domain 157..176 /note="transmembrane domain"

XX WO200144293-A2.

XX 21-JUN-2001.

XX 14-DEC-2000; 2000WO-GB004802.

XX 17-DEC-1999; 99GB-00029970.

XX (GLAXO ) GLAXO GROUP LTD.

XX Plimpton M, Powell AJ, Sauseau P;

XX WPI; 2001-398129/42.

XX N-PSDB; AAF84146.

XX Novel sub-unit for voltage-gated sodium channel proteins for producing

XX agents useful for treating pain.

XX Claim 1; Fig 2; 31pp; English.

CC The invention provides a novel betal-like sub-unit for voltage-gated

CC sodium ion channel polypeptide, specifically a sensory neurone specific

CC channel (SNS) subunit. The novel betal-like subunit is useful for

CC The subunit can be expressed by standard recombinant methodology. The  
CC present sequence represents a human novel sodium channel betal-like  
CC subunit  
XX

XX Sequence 215 AA;

Query Match . . . 100.0%; Score 1124; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2,4e-98;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYVWSVCFPVCEVPSSETEAQGNPKMRLRCISCKKREVEATTIV 60  
DB 1 MPAFNRLLPLASLVLIYVWSVCFPVCEVPSSETEAQGNPKMRLRCISCKKREVEATTIV 60  
QY 61 EMFYRPEGKDFLIYEYRNGHOEVSPFOGRLQWNGSKDLDVSTIVNTLNDGGLTTC 120  
DB 61 EMFYRPEGKDFLIYEYRNGHOEVSPFOGRLQWNGSKDLDVSTIVNTLNDGGLTTC 120  
QY 121 NVSRREFEFAHRPFVKTRRLIPLRVTEBAGEDFTSVSEIMMYILLVFLTMLLLEMTYC 180  
DB 121 NVSRREFEFAHRPFVKTRRLIPLRVTEBAGEDFTSVSEIMMYILLVFLTMLLLEMTYC 180  
QY 181 YRKVSKAEBAQAQENASDYLAIPSENKENSAPVVEE 215  
DB 181 YRKVSKAEBAQAQENASDYLAIPSENKENSAPVVEE 215

RESULT 3

ABB05689  
ID ABB05689 standard; protein; 215 AA.

XX ABB05689;

XX 30-APR-2002 (first entry)

DE Human signal transduction protein clone amy2\_2118.

XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;

KW gene therapy.

XX Homo sapiens.

XX WO200198454-A2.

XX 27-DEC-2001.

XX 25-APR-2001; 2001WO-IB002050.

XX 25-APR-2000; 2000US-0199380P.

XX (GEHU-) GERMAN HUMAN GENOME PROJECT.

XX Wiemann S;

XX WPI; 2002-055860/07.

XX N-PSDB; ABA93727.

XX Human cDNA sequences and clones derived from human fetal brain, fetal

XX kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic

XX screening and therapy.

XX Claim 1; Page 176; 611pp; English.

CC The present invention describes assemblages and computer readable media

CC comprising novel human cDNA sequences and clones derived from human

CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA

CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the

CC present invention which encode the proteins given in ABB05662 to

XX  
SQ Sequence 215 AA;

Query Match 100.0%; Score 1124; DB 5; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2,4e-98;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANRLPLASLVLIVWVCPVCVEPSETEAVOGNPMKRCISCMKREBEATTV 60  
DB 1 MPANRLPLASLVLIVWVCPVCVEPSETEAVOGNPMKRCISCMKREBEATTV 60  
QY 61 EWFYRPGKDFLIYERNHQEVESPFQGRLOMNGSKDQDVSITVLTNDLSDGLYTC 120  
DB 61 EWFYRPGKDFLIYERNHQEVESPFQGRLOMNGSKDQDVSITVLTNDLSDGLYTC 120  
QY 121 NVSREFFEHARPPVKTRTLPRLVTEAGEDEFTSVSEIMMYTLVFTLMLIEMIYC 180  
DB 121 NVSREFFEHARPPVKTRTLPRLVTEAGEDEFTSVSEIMMYTLVFTLMLIEMIYC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215

RESULT 4  
AAE35366  
ID AAE35366 standard; protein: 215 AA.

AC AAE35366;  
DT 17-JUN-2003 (first entry)

DE Human sodium channel beta-3 subunit.

XX Human; sodium channel beta-3 subunit; 98359 protein; gene therapy; AIDS;  
KM shock; hypertension; psychiatric disease; obsessive-compulsive disorder;  
KM bipolar affective disorder; attention deficit disorder; phobic disorder;  
KM cardiovascular disorder; neurological disorder; spinocerebellar ataxia;  
KM Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;  
KM autoimmune disorder; cellular proliferative disorder; Krabbe's disease;  
KM metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;  
KM bone metabolism disorder; endothelial cell disorder; viral encephalitis;  
KM acquired immune deficiency syndrome; peripheral neuropathy; arrhythmia;  
KM poliomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;  
KM dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;  
KM pain.

XX Homo sapiens.

OS  
XX  
FH Key Location/Qualifiers  
FT Domain 38..70  
FT /note= "Conserved motif"  
FT Domain 104..122  
FT /note= "Conserved motif"

PN EPI258495-A1.

XX 20-NOV-2002.

XX 09-MAY-2002; 2002BP-00253262.

XX 09-MAY-2001; 2001US-0289893P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis Raj;

XX WPI; 2003-185859/19.

XX New isolated human sodium channel beta-4 subunit nucleic acid molecule  
PT and polypeptide, useful for diagnosing and treating disorders with  
PT aberrant beta-4 subunit function or expression, such as neurological and  
PT cardiovascular diseases.

XX  
PS Disclosure; Page 55-56; 62pp; English.

XX The invention relates to human sodium channel beta-4 subunit, 98359  
CC polypeptides and polynucleotides. The methods and compositions of the  
CC invention are useful for diagnosing, screening and treating disorders  
CC associated with aberrant or deficient sodium channel beta-4 subunit  
CC function or expression such as paroxysmal congenital, hyperkalemic  
CC periodic paralysis, epilepsy, psychiatric diseases (anxiety or phobic  
CC disorders, attention deficit disorder, obsessive-compulsive disorder and  
CC bipolar affective disorder), dementia, cardiovascular disorders  
CC (hypertension, shock, heart failure, arrhythmias and cardiomyopathy),  
CC neurodegenerative disorders (Alzheimer's or Parkinson's disease,  
CC spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders  
CC (diabetes, arthritis), cellular proliferative disorders (cancer), bone  
CC metabolism disorders, liver disorders, viral infections (AIDS, rabies,  
CC herpes simplex, poliomyelitis, viral encephalitis and peripheral  
CC neuropathy), endothelial cell disorders, demyelinating diseases (multiple  
CC sclerosis), pain and/or metabolic disorders (leukodystrophies, Krabbe's  
CC disease and Leigh disease). Polynucleotides of the invention are used to  
CC identify an individual from a biological sample (tissue typing), and in  
CC forensic identification of a biological sample. The invention is useful  
CC in gene therapy. The present sequence is human sodium channel beta-3  
CC subunit. This sequence is used in the invention

XX  
SQ Sequence 215 AA;

Query Match 100.0%; Score 1124; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2,4e-98;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANRLPLASLVLIVWVCPVCVEPSETEAVOGNPMKRCISCMKREBEATTV 60  
DB 1 MPANRLPLASLVLIVWVCPVCVEPSETEAVOGNPMKRCISCMKREBEATTV 60  
QY 61 EWFYRPGKDFLIYERNHQEVESPFQGRLOMNGSKDQDVSITVLTNDLSDGLYTC 120  
DB 61 EWFYRPGKDFLIYERNHQEVESPFQGRLOMNGSKDQDVSITVLTNDLSDGLYTC 120  
QY 121 NVSREFFEHARPPVKTRTLPRLVTEAGEDEFTSVSEIMMYTLVFTLMLIEMIYC 180  
DB 121 NVSREFFEHARPPVKTRTLPRLVTEAGEDEFTSVSEIMMYTLVFTLMLIEMIYC 180  
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215

RESULT 5

ABR83183  
ID ABR83183 standard; protein: 215 AA.

AC ABR83183;

DT 15-JAN-2004 (first entry)

XX Human SCN3B protein.

XX SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;  
KM neuroprotective; anesthetic; cytosolic; cerebroprotective; cardiac;  
KM hypotensive; gene therapy; SCN3B, human.

XX Homo sapiens.

XX WO2003072751-A2.

XX 04-SEP-2003.

XX 25-FEB-2003; 2003MO-US006010.

XX 25-FEB-2002; 2002US-0359382P.

XX (UYVA-) UNIV VANDERBILT.

XX George AL, Lossin C;  
 XX WPI: 2003-712725/67.  
 DR N-PSDB; ACR57870.  
 XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in  
 PT screening for modulators, for treating e.g. epilepsy.  
 XX  
 XX Disclosure; Page 145-147, 176pp; English.  
 XX  
 XX The invention relates to a recombinantly expressed and isolated human  
 CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally  
 CC incorporated into a cell, is used to screen for specific modulators,  
 CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,  
 CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic  
 CC epilepsy of infancy, stroke, cardiac arrest, hyperalemic paralysis,  
 CC motor endplate diseases, hypertension, congestive heart failure and  
 CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic  
 CC and metastatic cancer cell lines). These activities can also be provided  
 CC by gene therapy vectors that express (I) or the modulators. The  
 CC modulators, also antibodies directed against (I), are used to detect  
 CC sodium channel polypeptides. The present sequence represents a human  
 CC SCN3B protein  
 CC  
 XX Sequence 215 AA;  
 SQ

Query Match 100.0%; Score 1124; DB 7; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-98;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLIVLYWVSCFPCVCEVPSSETAEOGPMKLRICSMKREBEATTIV 60  
 DB 1 MPAFRLPLASLIVLYWVSCFPCVCEVPSSETAEOGPMKLRICSMKREBEATTIV 60  
 QY 61 EMFYRPEGKDFLIYENRGHGVESPFQGRLOMNGSKDLOVSTIVLVNTLNDGLTYC 120  
 DB 61 EMFYRPEGKDFLIYENRGHGVESPFQGRLOMNGSKDLOVSTIVLVNTLNDGLTYC 120  
 QY 121 NVSRREFEFARHPFYKTRRLIPLRYTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
 DB 121 NVSRREFEFARHPFYKTRRLIPLRYTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
 QY 181 YRKVSKAEBAEQENASDYLAIPSENKENSAPVEE 215  
 DB 181 YRKVSKAEBAEQENASDYLAIPSENKENSAPVEE 215

RESULT 6  
 AAB36001  
 ID AAB36001 standard; protein; 215 AA.  
 XX  
 AC AAB36001;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Rat beta3 subunit.  
 XX  
 XX Rat, beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;  
 KM vasodilator; cardiac; nootropic; cytostatic; dermatological;  
 KM gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;  
 KM ischaemia; heart disease; Jacobsen Syndrome;  
 KM familial nonchromaffin paraganglioma; phenylketonuria;  
 KM Charcot Marie Tooth disease.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200063367-A1.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 24-FEB-2000; 2000WO-EP001783.  
 XX

PR 15-APR-1999; 99US-0129473P.  
 XX  
 XX (WARN ) WARNER LAMBERT CO.  
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
 XX  
 XX Cox P, Dixon A, Jackson A, Morgan K;  
 PI WPI: 2000-665241/64.  
 DR N-PSDB; AAC67836.  
 XX  
 XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium  
 PT channel, and their corresponding polypeptides, useful for detecting and  
 PT treating sodium channel-associated conditions, e.g. pain, epilepsy and  
 PT stroke.  
 XX  
 XX Claim 33; Fig 4; 88pp; English.  
 XX  
 XX The present sequence is given in the claims of a specification relating  
 CC to a novel family of beta sub-unit proteins from a voltage-gated sodium  
 CC channel. Human and rat beta sub-units, which have been collectively  
 CC identified as beta3, have been isolated. The polynucleotides and  
 CC polypeptides are useful for screening for agonists and antagonists of  
 CC sodium channels. The agonists, antagonists, proteins and nucleic acids  
 CC may be used diagnosing of treating diseases or conditions associated with  
 CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,  
 CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,  
 CC Phenylketonuria and Charcot Marie Tooth disease  
 CC  
 XX Sequence 215 AA;  
 SQ

Query Match 98.3%; Score 1105; DB 3; Length 215;  
 Best Local Similarity 98.1%; Pred. No. 1.5e-96;  
 Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLIVLYWVSCFPCVCEVPSSETAEOGPMKLRICSMKREBEATTIV 60  
 DB 1 MPAFRLPLASLIVLYWVSCFPCVCEVPSSETAEOGPMKLRICSMKREBEATTIV 60  
 QY 61 EMFYRPEGKDFLIYENRGHGVESPFQGRLOMNGSKDLOVSTIVLVNTLNDGLTYC 120  
 DB 61 EMFYRPEGKDFLIYENRGHGVESPFQGRLOMNGSKDLOVSTIVLVNTLNDGLTYC 120  
 QY 121 NVSRREFEFARHPFYKTRRLIPLRYTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
 DB 121 NVSRREFEFARHPFYKTRRLIPLRYTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
 QY 181 YRKVSKAEBAEQENASDYLAIPSENKENSAPVEE 215  
 DB 181 YRKVSKAEBAEQENASDYLAIPSENKENSAPVEE 215

RESULT 7  
 AAB50243  
 ID AAB50243 standard; protein; 215 AA.  
 XX  
 AC AAB50243;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Rat sodium channel beta3 protein Alrx94h5.  
 XX  
 XX Rat, sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;  
 KM Rat, sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;  
 KM neurodegenerative disorder; mood disorder; muscle contraction.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200069912-A1.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 12-MAY-2000; 2000WO-US013144.  
 XX  
 PR 14-MAY-1999; 99US-0134198P.  
 XX

XX (MILL-) MILLENNIUM PHARM INC.  
 PA Curtis RAJ;  
 PI WPI; 2001-122743/13.  
 XX N-PSDB; AAC90600.  
 DR  
 XX  
 PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal  
 PT root ganglion cDNA library for use in chromosome mapping, forensic  
 PT medicine, monitoring clinical trials and therapeutics.  
 XX  
 PS Claim 9; Fig 2; 145bp; English.  
 CC  
 CC The present invention provides the protein and coding sequences of the  
 CC rat sodium channel beta-3 protein, designated Altra945. This protein is  
 CC involved in the generation of pain and other sensory or perceptible nerve  
 CC impulses, in the establishment and endurance of mood, neurodegenerative  
 CC and sleep disorders, and in the control of muscle contraction, including  
 CC movements such as the heartbeat, digestion and vascular tone. The  
 CC sequences can be used in predictive medicine, screening and diagnostic  
 CC assays, and in pharmacogenomics  
 XX  
 SQ Sequence 215 AA;  
 Query Match 98.3%; Score 1105; DB 4; Length 215;  
 Best Local Similarity 98.1%; Pred. No. 1.5e-96;  
 Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MPANRLPLASIVLIYWSVCPVCEVPSSETEAVQGNPMKLRCSCKMREVEATTV 60  
 Db 1 MPANRLPLASIVLIYWSVCPVCEVPSSETEAVQGNPMKLRCSCKMREVEATTV 60  
 QY 61 EWFYRPGGKDFLIYERNRNGHGVESPPQGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120  
 Db 61 EWFYRPGGKDFLIYERNRNGHGVESPPQGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120  
 QY 121 NVSRREFEFAHNPFPVKTTLIPLRVTEEGEDFTSVSSIMTYILLVFLTMLFIEMTYC 180  
 Db 121 NVSRREFEFAHNPFPVKTTLIPLRVTEEGEDFTSVSSIMTYILLVFLTMLFIEMTYC 180  
 QY 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215  
 Db 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215  
 RESULT 8  
 ID AAE35367 standard; protein; 215 AA.  
 XX  
 AC AAE35367;  
 XX  
 DT 17-JUN-2003 (first entry)  
 XX  
 DE Rat sodium channel beta-3 subunit.  
 XX  
 KM Rat; sodium channel beta-3 subunit; 98359 protein; gene therapy; AIDS;  
 KM shock; hypertension; psychiatric disease; obsessive-compulsive disorder;  
 KM bipolar affective disorder; attention deficit disorder; phobic disorder;  
 KM cardiovascular disorder; neurological disorder; spinocerebellar ataxia;  
 KM Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;  
 KM autoimmune disorder; cellular proliferative disorder; Krabbe's disease;  
 KM metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;  
 KM bone metabolism disorder; endothelial cell disorder; viral encephalitis;  
 KM acquired immune deficiency syndrome; peripheral neuropathy; arhythmia;  
 KM polioomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;  
 KM dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;  
 KM pain.  
 XX  
 OS Rattus norvegicus.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 68..64

PT /note="Conserved motif"  
 FT Domain 104..122  
 PT /note="Conserved motif"  
 XX  
 PN EPI258495-A1.  
 XX  
 PD 20-NOV-2002.  
 XX  
 PF 09-MAY-2002; 2002EP-00253262.  
 XX  
 PR 09-MAY-2001; 2001US-0289893P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Curtis RAJ;  
 XX  
 DR WPI; 2003-185859/19.  
 XX  
 PT New isolated human sodium channel beta-4 subunit nucleic acid molecule  
 PT and polypeptide, useful for diagnosing and treating disorders with  
 PT aberrant beta-4 subunit function or expression, such as neurological and  
 PT cardiovascular diseases.  
 XX  
 PS Disclosure; Page 56; 62pp; English.  
 XX  
 CC The invention relates to human sodium channel beta-4 subunit, 98359  
 CC polypeptides and polynucleotides. The methods and compositions of the  
 CC invention are useful for diagnosing, screening and treating disorders  
 CC associated with aberrant or deficient sodium channel beta-4 subunit  
 CC function or expression such as paramyotonia congenital, hyperkalaemic  
 CC periodic paralysis, epilepsy, psychiatric diseases (anxiety or phobic  
 CC disorders, attention deficit disorder, obsessive-compulsive disorder and  
 CC bipolar affective disorder), dementia, cardiovascular disorders  
 CC (hypertension, shock, heart failure, arhythmias and cardiomyopathy),  
 CC neurological disorders (Alzheimer's or Parkinson's disease,  
 CC spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders  
 CC (diabetes, arthritis), cellular proliferative disorders (cancer), bone  
 CC metabolism disorders, liver disorders, viral infections (AIDS, rabies,  
 CC herpes simplex, polioyelitis, viral encephalitis and peripheral  
 CC neuropathy), endothelial cell disorders, demyelinating diseases (multiple  
 CC sclerosis), pain and/or metabolic disorders (leukodystrophies, Krabbe's  
 CC disease and Leigh disease). Polynucleotides of the invention are used to  
 CC identify an individual from a biological sample (tissue typing), and in  
 CC forensic identification of a biological sample. The invention is useful  
 CC in gene therapy. The present sequence is rat sodium channel beta-3  
 CC subunit. This sequence is used in the invention  
 XX  
 SQ Sequence 215 AA;  
 Query Match 98.3%; Score 1105; DB 6; Length 215;  
 Best Local Similarity 98.1%; Pred. No. 1.5e-96;  
 Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MPANRLPLASIVLIYWSVCPVCEVPSSETEAVQGNPMKLRCSCKMREVEATTV 60  
 Db 1 MPANRLPLASIVLIYWSVCPVCEVPSSETEAVQGNPMKLRCSCKMREVEATTV 60  
 QY 61 EWFYRPGGKDFLIYERNRNGHGVESPPQGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120  
 Db 61 EWFYRPGGKDFLIYERNRNGHGVESPPQGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120  
 QY 121 NVSRREFEFAHNPFPVKTTLIPLRVTEEGEDFTSVSSIMTYILLVFLTMLFIEMTYC 180  
 Db 121 NVSRREFEFAHNPFPVKTTLIPLRVTEEGEDFTSVSSIMTYILLVFLTMLFIEMTYC 180  
 QY 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215  
 Db 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215  
 RESULT 9  
 ID AAM79212 standard; protein; 195 AA.  
 XX

XX AAM79212;  
AC  
XX 06-NOV-2001 (first entry)  
DT  
XX Human protein SEQ ID NO 1874.  
DE  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation.  
XX Homo sapiens.  
OS  
XX WO200157190-A2.  
PN  
XX 09-AUG-2001.  
PD  
XX 05-FEB-2001; 2001WO-US004098.  
PF  
XX 03-FEB-2000; 2000US-00496914.  
PR 27-APR-2000; 2000US-00560875.  
PR 20-JUN-2000; 2000US-00598075.  
PR 19-JUL-2000; 2000US-00620325.  
PR 01-SEP-2000; 2000US-00654936.  
PR 15-SEP-2000; 2000US-00663561.  
PR 20-OCT-2000; 2000US-00693325.  
PR 30-NOV-2000; 2000US-00728422.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX WPI: 2001-476283/51.  
DR N-PSDB; AAK52345.  
XX  
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful  
PT in diagnosis and gene therapy.  
XX  
PS Claim 20; Page 4260; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
XX encoded polypeptides (AAM7923-AAK80102) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulatory  
CC activity, tissue growth factor activity, immunomodulatory activating and  
CC activity/inhibit activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Notes: Records for SEQ ID NO 2110 (AAK52581), 2111  
CC (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the  
CC sequence listing were missing at the time of publication  
XX  
SQ Sequence 195 AA;  
Query Match 91.1%; Score 1024; DB 4; Length 195;  
Best Local Similarity 100.0%; Pred. No. 6.7e-89;  
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 NVSRFEFEARHPVKTTRLLPLRVTEAGEDFTSVSEIMMYILLVFLTLLIEMIYC 180  
OY 181 YRKVSKAEAAQENA 195  
DB 181 YRKVSKAEAAQENA 195  
RESULT 10  
AAB50245  
ID AAB50245 standard; protein, 191 AA.  
XX  
AC AAB50245;  
XX  
DT 13-MAR-2001 (first entry)  
DE Rat sodium channel beta3 protein Alrx94h5 mature protein.  
XX  
KW Rat; sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;  
KW neurodegenerative disorder; mood disorder; muscle contraction.  
XX  
OS Rattus sp.  
XX  
XX WO200069912-A1.  
PN  
XX 23-NOV-2000.  
PD  
XX 12-MAY-2000; 2000WO-US013144.  
PF  
XX 14-MAY-1999; 99US-0134198P.  
PR  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX Curtis RAD;  
XX  
PI WPI: 2001-122743/13.  
PI N-PSDB; AAC90600.  
DR  
XX  
XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal  
PT root ganglion cDNA library for use in chromosome mapping, forensic  
PT medicine, monitoring clinical trials and therapeutics.  
XX  
XX Claim 9; Fig 2; 145pp; English.  
XX  
XX The present invention provides the protein and coding sequences of the  
CC rat sodium channel beta3 protein, designated Alrx94h5. This protein is  
CC involved in the generation of pain and other sensory or perceptible nerve  
CC impulses, in the establishment and endurance of mood, neurodegenerative  
CC and sleep disorders, and in the control of muscle contraction, including  
CC movements such as the heartbeat, digestion and vascular tone. The  
CC sequences can be used in predictive medicine, screening and diagnostic  
CC assays, and in pharmacogenomics  
XX  
SQ Sequence 191 AA;  
Query Match 87.7%; Score 986; DB 4; Length 191;  
Best Local Similarity 99.0%; Pred. No. 2.6e-85;  
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



## RESULT 11

ABG22577  
ID ABG22577 standard; protein: 369 AA.

AC ABG22577;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22568.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;

PI WPI; 2001-639362/73.

DR N-PSDB; AAS86764.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

PS Claim 20; SEQ ID NO 52936; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX sequences. (I) is useful as hybridisation probes, polymerase chain  
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX and in recombinant production of (II). The polynucleotides are also used  
XX in diagnostics as expressed sequence tags for identifying expressed  
XX genes. (I) is useful in gene therapy techniques to restore normal  
XX activity of (II) or to treat disease states involving (II). (II) is  
XX useful for generating antibodies against it, detecting or quantitating a  
XX polypeptide in tissue, as molecular weight markers and as a food  
XX supplement. (II) and its binding partners are useful in medical imaging  
XX of sites expressing (II). (I) and (II) are useful for treating disorders  
XX involving aberrant protein expression or biological activity. The  
XX polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic  
XX amino acid sequences of the invention. Note: The sequence data for this  
XX patent did not appear in the printed specification, but was obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

SO Sequence 369 AA;

Query Match 83.9%; Score 942.5; DB 4; Length 369;

Best Local Similarity 93.9%; Pred. No. 8.1e-81;  
Matches 184; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 MPAFNLFPLASIVLIYWSVCPVCVEVSETEA-VQGNPMKLRCSCKRREVEATTYV 59

DB 127 MPAFNLFPLASIVLIYWSVCPVCVEVSETEA-VQGNPMKLRCSCKRREVEATTYV 186

QY 60 VEWFYRPEGKDFLIYVRNGHVESPFQGRLOWNGSKDLOVSIIVLVNTINDSLTYT 119

DB 187 VEWFYRPEGKDFLIYVRNGHVESPFQGRLOWNGSKDLOVSIIVLVNTINDSLTYT 246

QY 120 CNVSRREFEFAHNPFKTTLPLRLVTEEGEDPTSVSISIMYIILLVLTLLIMIX 179

DB 247 CNVSRREFEFAHNPFKTTLPLRLVTEEGEDPTSVSISIMYIILLVLTLLIMIX 306

QY 180 CYRKVSKEEPAQENA 195

DB 307 CYRKVSKEEPAQENA 322

## RESULT 12

AAB36020  
ID AAB36020 standard; protein: 159 AA.

AC AAB36020;

DT 15-FEB-2001 (first entry)

DE Human beta3 subunit peptide, SEQ ID NO: 22.

KW Human; beta sub-unit; beta3; analgesic; anticonvulsant;  
KW cerebroprotective; vasotropic; cardiant; nootropic; cyostatic;  
KW dermatological; gene therapy; voltage-gated sodium channel; pain;  
KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;  
KW familial nonchromaffin paraganglioma; phenylketonuria;  
KW Charcot Marie Tooth disease.

OS Homo sapiens.

PN WO200063367-A1.

PD 26-OCT-2000.

PF 24-FEB-2000; 2000WO-EP001783.

PR 15-APR-1999; 99US-0129473P.

PA (WARN) WARNER LAMBERT CO.  
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI Cox P, Dixon A, Jackson A, Morgan K;

PI WPI; 2000-665241/64.

DR Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium  
XX channel, and their corresponding polypeptides, useful for detecting and  
XX treating sodium channel-associated conditions, e.g. pain, epilepsy and  
XX stroke.

PS Claim 36; Page 76; 88pp; English.

XX The present sequence is given in the claims of a specification relating  
XX to a novel family of beta sub-unit proteins from a voltage-gated sodium  
XX channel. Human and rat beta sub-units, which have been collectively  
XX identified as beta3, have been isolated. The polynucleotides and  
XX polypeptides are useful for screening for agonists and antagonists of  
XX sodium channels. The agonists, antagonists, proteins and nucleic acids  
XX may be used diagnosing of treating diseases or conditions associated with  
XX voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,  
XX heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,  
XX phenylketonuria and Charcot Marie Tooth disease

SO Sequence 159 AA;

Query Match 75.0%; Score 843; DB 3; Length 159;

Best Local Similarity 100.0%; Pred. No. 7.9e-72;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNLFPLASIVLIYWSVCPVCVEVSETEA-VQGNPMKLRCSCKRREVEATTYV 60

DB 1 MPAFNLFPLASIVLIYWSVCPVCVEVSETEA-VQGNPMKLRCSCKRREVEATTYV 60

QY 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120  
DB 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120  
QY 121 NVSRFEFEARHPVVKTRLLIPLRVTEBAGDFTSVSE 159  
DB 121 NVSRFEFEARHPVVKTRLLIPLRVTEBAGDFTSVSE 159

## RESULT 13

ADSI0835  
ID ADSI0835 standard; protein, 157 AA.

AC ADSI0835;

DT 16-DEC-2004 (first entry)

DE Human therapeutic protein - SEQ ID 1072.

KM antiinflammatory; neuroprotective; antinaemic; cyrostatic; vulnerary;  
inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
aplastic anaemia; cancer; wound healing; gene therapy.

KM aplastic anaemia; cancer; wound healing; gene therapy.

OS Homo sapiens.

PN WO2004080148-A2.

PD 23-SEP-2004.

PF 30-SEP-2003; 2003WO-US030720.

PR 02-OCT-2002; 2002US-0416186P.

PA (NUVE-) NUVELO INC.

PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y,  
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

DR MPI: 2004-668857/65.

DR N-PsDB; ADSI0151.

PT New polynucleotide, useful in preparing a composition for diagnosing or  
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
PT aplastic anemia or cancer for promoting wound healing.

PS Claim 20; SEQ ID NO 1072; 718bp; English.

CC The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antinaemic, cyrostatic and vulnerary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC disorders, such as aplastic anaemia or cancer, as well as for promoting  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic protein  
CC of the invention. The current sequence is not shown explicitly within the  
CC specification but can be accessed from the WIPO web-site.

XX Sequence 157 AA;

XX Query Match 74.2%; Score 834; DB 8; Length 157;

XX Best Local Similarity 100.0%; Pred. No. 5.6e-71;

XX Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAENRLPPLASLVIIYVSVCPVCVEVPSETEAVQGNPKMRLCISCKREBEVATTVV 60  
DB 1 MPAENRLPPLASLVIIYVSVCPVCVEVPSETEAVQGNPKMRLCISCKREBEVATTVV 60

QY 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120  
DB 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120

QY 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120  
DB 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120

QY 121 NVSRFEFEARHPVVKTRLLIPLRVTEBAGDFTSVV 157  
DB 121 NVSRFEFEARHPVVKTRLLIPLRVTEBAGDFTSVV 157

## RESULT 14

AAB36021  
ID AAB36021 standard; protein, 159 AA.

AC AAB36021;

DT 15-FEB-2001 (first entry)

DE Rat beta3 subunit peptide, SEQ ID NO: 23.

KM Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;  
vasotropic; cardiac; nootropic; cyrostatic; dermatological;  
gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;  
ischemia; heart disease; Jacobsen Syndrome;  
familial nonchromaffin paraganglioma; phenylketonuria;  
Charcot Marie Tooth disease.

KM Charcot Marie Tooth disease.

OS Rattus sp.

PN WO200063367-A1.

PD 26-OCT-2000.

PF 24-FEB-2000; 2000WO-EP001783.

PR 15-APR-1999; 99US-0129473P.

PA (WARIN ) WARNER LAMBERT CO.  
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI Cox P, Dixon A, Jackson A, Morgan K;

PI MPI: 2000-665241/64.

DR MPI: 2000-665241/64.

XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium  
XX channel, and their corresponding polypeptides, useful for detecting and  
XX treating sodium channel-associated conditions, e.g. pain, epilepsy and  
XX stroke.

PT Claim 36; Page 76-77; 88bp; English.

PS The present sequence is given in the claims of a specification relating  
PS to a novel family of beta sub-unit proteins from a voltage-gated sodium  
PS channel. Human and rat beta sub-units, which have been collectively  
PS identified as beta3, have been isolated. The polynucleotides and  
PS polypeptides are useful for screening for agonists and antagonists of  
PS sodium channels. The agonists, antagonists, proteins and nucleic acids  
PS may be used diagnosing of treating diseases or conditions associated with  
PS voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,  
PS heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,  
PS Phenylketonuria and Charcot Marie Tooth disease

XX Sequence 159 AA;

XX Query Match 74.0%; Score 832; DB 3; Length 159;

XX Best Local Similarity 98.7%; Pred. No. 8.8e-71;

XX Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPAENRLPPLASLVIIYVSVCPVCVEVPSETEAVQGNPKMRLCISCKREBEVATTVV 60  
DB 1 MPAENRLPPLASLVIIYVSVCPVCVEVPSETEAVQGNPKMRLCISCKREBEVATTVV 60

QY 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120  
DB 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120

QY 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120  
DB 61 EMFYRPEGKDFLIYENRNGHOEVESPFQGRLOWNGSKDLOVSIITVNTVLTNDGSLVTC 120

QY 121 NVSRFEFEARHPVVKTRLLIPLRVTEBAGDFTSVSE 159  
DB 121 NVSRFEFEARHPVVKTRLLIPLRVTEBAGDFTSVSE 159

DB 121 N/SEFEFEARBPVXTRRLIPLRVTEAGEDEFTSVSE 159

RESULT 15

ABG22576  
ID ABG22576 standard; protein; 1176 AA.

XX  
AC ABG22576;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22567.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB; AAS66763.

XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX Claim 20; SEQ ID NO 52935; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC or sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1176 AA;

Query Match 61.7%; Score 694; DB 4; Length 1176;  
Best Local Similarity 100.0%; Pred. No. 1.3e-56;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSVCFPVCEVBPSETAVQGNPKLRICISCMKREBEVATTVEFYPBEGKDFLIYEYR 78  
DB 987 VSVCFPVCEVBPSETAVQGNPKLRICISCMKREBEVATTVEFYPBEGKDFLIYEYR 1046

QY 79 NGHVEVSPFQGRLOVNSKDLQDVSIIVLNTVLTNDSGLYTCNVSRFEFEARPPVKT 138  
DB 1047 NGHVEVSPFQGRLOVNSKDLQDVSIIVLNTVLTNDSGLYTCNVSRFEFEARPPVKT 1106  
QY 139 RLIPLRTEE 148  
DB 1107 RLIPLRTEE 1116

Search completed: March 31, 2005, 20:17:51  
Job time : 124.5 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:11:14 ; Search time 30 Seconds  
(without alignments)  
534.985 Million cell updates/sec

Title: US-09-977-579-2

Perfect score: 1124

Sequence: 1 MPANRFLPLASLVLYWVS.....SDYLAIPEKNSAVPVEE 215

Scoring table: BLOSUM62

Searched: Gap0 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*

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6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	41.8	204	US-09-949-016-8240	Sequence 8240, Ap
2	147	13.1	215	US-09-949-016-6658	Sequence 6658, Ap
3	147	13.1	263	US-09-949-016-10819	Sequence 10819, A
4	131	11.7	269	US-09-430-503-2	Sequence 2, Appli
5	131	11.7	269	US-09-430-503-4	Sequence 4, Appli
6	131	11.7	269	US-09-430-503-6	Sequence 6, Appli
7	131	11.7	269	US-09-430-503-8	Sequence 8, Appli
8	131	11.7	313	US-09-949-016-10974	Sequence 10974, A
9	129	11.5	199	US-09-430-503-44	Sequence 44, Appl
10	129	11.5	199	US-09-430-503-48	Sequence 48, Appl
11	127	11.3	199	US-09-430-503-42	Sequence 42, Appl
12	127	11.3	199	US-09-430-503-46	Sequence 46, Appl
13	127	11.3	209	US-09-430-503-18	Sequence 18, Appl
14	127	11.3	209	US-09-430-503-20	Sequence 20, Appl
15	127	11.3	209	US-09-430-503-22	Sequence 22, Appl
16	127	11.3	209	US-09-430-503-24	Sequence 24, Appl
17	125	11.1	270	US-09-430-503-26	Sequence 26, Appl
18	125	11.1	270	US-09-430-503-28	Sequence 28, Appl
19	125	11.1	270	US-09-430-503-30	Sequence 30, Appl
20	125	11.1	270	US-09-430-503-32	Sequence 32, Appl
21	118	10.5	159	US-09-430-503-34	Sequence 34, Appl
22	118	10.5	159	US-09-430-503-36	Sequence 36, Appl
23	118	10.5	159	US-09-430-503-38	Sequence 38, Appl
24	118	10.5	159	US-09-430-503-40	Sequence 40, Appl
25	112.5	9.8	215	US-09-949-016-6523	Sequence 6523, Ap
26	110.5	9.8	225	US-09-949-016-10820	Sequence 10820, A
27	110.5	9.8	225	US-09-949-016-10820	Sequence 10820, A

28	109	9.7	344	US-09-656-952-19	Sequence 19, Appl
29	109	9.7	394	US-09-656-952-20	Sequence 20, Appl
30	109	9.7	394	US-09-855-323-17	Sequence 17, Appl
31	108	9.6	801	US-09-383-630-6	Sequence 6, Appli
32	106	9.4	519	US-08-996-338-21	Sequence 21, Appl
33	106	9.4	519	US-09-556-972-21	Sequence 21, Appl
34	106	9.4	537	US-08-604-333-4	Sequence 4, Appli
35	106	9.4	537	US-09-110-618-4	Sequence 4, Appli
36	106	9.4	537	US-09-173-151A-29	Sequence 29, Appl
37	106	9.4	537	US-09-578-178-4	Sequence 4, Appli
38	106	9.4	537	US-09-577-806-4	Sequence 4, Appli
39	106	9.4	537	US-09-621-502-8	Sequence 8, Appli
40	99.5	8.9	471	US-09-949-016-9042	Sequence 9042, Ap
41	99.5	8.9	471	US-09-949-016-9043	Sequence 9043, Ap
42	99.5	8.9	471	US-09-949-016-9044	Sequence 9044, Ap
43	99.5	8.9	471	US-09-949-016-9045	Sequence 9045, Ap
44	99.5	8.9	471	US-09-949-016-9046	Sequence 9046, Ap
45	99.5	8.9	471	US-09-949-016-9047	Sequence 9047, Ap

ALIGNMENTS

RESULT 1  
US-09-949-016-8240  
Sequence 8240, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 8240  
LENGTH: 204  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8240  
Query Match 41.8%; Score 470; DB 4; Length 204;  
Best Local Similarity 51.0%; Pred. No. 1.2e-42; Indels 8; Gaps 5;  
Matches 101; Conservative 30; Mismatches 59;  
QY 26 CVEVPSETEAAGNPMKLRICSCMKREVEATTVWFWYRPEGKQFL-IVRYRNGHOEV 84  
DB 7 CVDVSTETAVYGMTFKILICISCRSEETAETFTFPQKGTREEVKILRRENEVLQ 66  
QY 85 ESP--FQGRLOMNGS---KQLODVSTLVAVNTLNDGLTYCNVSRPEFAHHPFVKTR 139  
DB 67 EEBEREFGRVWVNGSRCTKLODLSIFITVTVNHSQDYCHVYRLFFPENYEHTSVVK 126  
QY 140 LIPLRVTEAAGEFTSVSEIMMYTLLVPLTLWLTLEMICYKRVSKA-EEAEOENASDY 198  
DB 127 KIHLEVDKNNRDMASIVSEIMMYTLLVPLTLWLVAMETICYKRIATETTAEOENASEY 186  
QY 199 LAIPSENKEN-SAVPVEE 215  
DB 187 LAITSEKENCCTGVQVAE 204  
RESULT 2  
US-09-949-016-6658  
Sequence 6658, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 6658  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6658

Query Match 13.1%; Score 147; DB 4; Length 215;  
Best Local Similarity 25.7%; Pred. No. 9.6e-08;  
Matches 57; Conservative 35; Mismatches 80; Indels 50; Gaps 9;

QY 7 LPLASLVLIYVWVSCFPVCEVPSBTEAVQGNPMKLRICSCMKREBEVATTVEWFPYRP 66  
DB 21 LMPILAA-VEIYTSRV-----LEAVNGTDARLKTCTSSPAPVGDALVT--WNFRP 67  
QY 67 -EGG-KDPLIYEYRNGHGVESPPQGRLOWNGSKLDQVSTIVLNTLNDGLTYCNVSR 124  
DB 68 LDGGEQGFVYHYHIDPQPMGRFRDYSWMDGNPERYASILMLKLPDQDNGTYCQVKN 127  
QY 125 EPEFAHRPFVKTTRLILPRTVEAGEDFTSVV-----SEIMMYILV-----FLTLML 173  
DB 128 -----PPDVGVIGETRLSVHTVRSEIHFLALAGSACALMIITVI 170  
QY 174 LIEMTYCYRKVSKAEAAQENASDYLAIPSENKENSAPVEE 215  
DB 171 VVLFQHYRKKRWABRA-----HKVVEIKSKEEBRLNOK 205

RESULT 3  
US-09-949-016-10819  
; Sequence 10819, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 10819  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10819

Query Match 13.1%; Score 147; DB 4; Length 263;  
Best Local Similarity 25.7%; Pred. No. 1.3e-07;  
Matches 57; Conservative 35; Mismatches 80; Indels 50; Gaps 9;

QY 7 LPLASLVLIYVWVSCFPVCEVPSBTEAVQGNPMKLRICSCMKREBEVATTVEWFPYRP 66  
DB 21 LMPILAA-VEIYTSRV-----LEAVNGTDARLKTCTSSPAPVGDALVT--WNFRP 67

DB 69 LMPILAA-VEIYTSRV-----LEAVNGTDARLKTCTSSPAPVGDALVT--WNFRP 115  
QY 67 -EGG-KDPLIYEYRNGHGVESPPQGRLOWNGSKLDQVSTIVLNTLNDGLTYCNVSR 124  
DB 116 LDGGEQGFVYHYHIDPQPMGRFRDYSWMDGNPERYASILMLKLPDQDNGTYCQVKN 175  
QY 125 EPEFAHRPFVKTTRLILPRTVEAGEDFTSVV-----SEIMMYILV-----FLTLML 173  
DB 176 -----PPDVGVIGETRLSVHTVRSEIHFLALAGSACALMIITVI 218  
QY 174 LIEMTYCYRKVSKAEAAQENASDYLAIPSENKENSAPVEE 215  
DB 219 VVLFQHYRKKRWABRA-----HKVVEIKSKEEBRLNOK 253

RESULT 4  
US-09-430-503-2  
; Sequence 2, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-2

Query Match 11.7%; Score 131; DB 3; Length 269;  
Best Local Similarity 23.0%; Pred. No. 7.1e-06;  
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVSSETEAVQGNPMKLRICSCMKREBEVATTVEWFPYRPGSKDLIYERYNGHQ 82  
DB 40 VYTRKEIRIVANGTGKLTLC-----KFKSITITGULTSVMSQPSGADTVSFFHSGQOV 95  
QY 83 EVES--PPQGRLOWNGSKLDQVSTIVLNTLNDGLTYCNVSRPEPEFAHRPFVKTTRL 140  
DB 96 YLGNYPPFKRDISWAGDLDKDKASINIENMOFHHNGTYICVKN----- 139  
QY 141 IPLRTEAGEDFTSVYSE-----IMMYILVFLTLMLIEMTYC--YRK----- 183  
DB 140 -PPDIVQPGHRIILVYVEKENLPVFPVWVVGIVAVLGLTLISMLAVLYRKRKSKR 198  
QY 184 -----YSKAEAAQENASD-----YLAIPSENKENSAPVEE 211  
DB 199 DYTGSTSESLSPVKQAPRKSPSDTEGLVYKSLPDSGSHGCPVI 240

RESULT 5  
US-09-430-503-4  
; Sequence 4, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-4

Query Match 11.7%; Score 131; DB 3; Length 269;  
Best Local Similarity 23.0%; Pred. No. 7.1e-06;  
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVSETEAVQGNPMKLCISCMKREVEAT--TVVEWYRPEGKDFL-IYEYRNGHQ 82  
DB 40 VYTPKEIFVANGOGKLTG---KFKSTSTGGLTSVMSFQEGADTVTSFHHYSGGV 95  
QY 83 EVES--PFOGRLOWNSKDLQDVSIYLVNTLNDGLYTCNVSRFEFEHRRPVKTRRL 140  
DB 96 YLGNYPFKRISWAGDLKKDASININEMQFIHNGTYICDVKN-----139  
QY 141 IPLRVTEAGEDFTSVSE-----IMMYILVFLTLLIEMIYC--YRK-----183  
DB 140 -PPDIVQPGHIRLYVEKENLPPFPVWVVGIVTAVVGLTLLISMLAVLYRRKNSKR 198  
QY 184 -----VSKAEBAQENASD---YLAIPSENKENSAY 211  
DB 199 DYTGCSTSESLSPVKAQPRKSPSDTEGLVKSLSFGSHQGPVI 240

RESULT 6  
US-09-430-503-6  
Sequence 6, Application US/09430503  
Patent No. 6355786  
GENERAL INFORMATION:  
APPLICANT: Zhao, Zhichuang  
TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2  
CURRENT APPLICATION NUMBER: US/09/430,503  
CURRENT FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 269  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-430-503-6

Query Match 11.7%; Score 131; DB 3; Length 269;  
Best Local Similarity 23.0%; Pred. No. 7.1e-06;  
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVSETEAVQGNPMKLCISCMKREVEAT--TVVEWYRPEGKDFL-IYEYRNGHQ 82  
DB 40 VYTPKEIFVANGOGKLTG---KFKSTSTGGLTSVMSFQEGADTVTSFHHYSGGV 95  
QY 83 EVES--PFOGRLOWNSKDLQDVSIYLVNTLNDGLYTCNVSRFEFEHRRPVKTRRL 140  
DB 96 YLGNYPFKRISWAGDLKKDASININEMQFIHNGTYICDVKN-----139  
QY 141 IPLRVTEAGEDFTSVSE-----IMMYILVFLTLLIEMIYC--YRK-----183  
DB 140 -PPDIVQPGHIRLYVEKENLPPFPVWVVGIVTAVVGLTLLISMLAVLYRRKNSKR 198  
QY 184 -----VSKAEBAQENASD---YLAIPSENKENSAY 211  
DB 199 DYTGCSTSESLSPVKAQPRKSPSDTEGLVKSLSFGSHQGPVI 240

RESULT 7  
US-09-430-503-8  
Sequence 8, Application US/09430503  
Patent No. 6355786  
GENERAL INFORMATION:  
APPLICANT: Zhao, Zhichuang  
TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2  
CURRENT APPLICATION NUMBER: US/09/430,503  
CURRENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 269  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-430-503-8

Query Match 11.7%; Score 131; DB 3; Length 269;  
Best Local Similarity 23.0%; Pred. No. 7.1e-06;  
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVSETEAVQGNPMKLCISCMKREVEAT--TVVEWYRPEGKDFL-IYEYRNGHQ 82  
DB 40 VYTPKEIFVANGOGKLTG---KFKSTSTGGLTSVMSFQEGADTVTSFHHYSGGV 95  
QY 83 EVES--PFOGRLOWNSKDLQDVSIYLVNTLNDGLYTCNVSRFEFEHRRPVKTRRL 140  
DB 96 YLGNYPFKRISWAGDLKKDASININEMQFIHNGTYICDVKN-----139  
QY 141 IPLRVTEAGEDFTSVSE-----IMMYILVFLTLLIEMIYC--YRK-----183  
DB 140 -PPDIVQPGHIRLYVEKENLPPFPVWVVGIVTAVVGLTLLISMLAVLYRRKNSKR 198  
QY 184 -----VSKAEBAQENASD---YLAIPSENKENSAY 211  
DB 199 DYTGCSTSESLSPVKAQPRKSPSDTEGLVKSLSFGSHQGPVI 240

RESULT 8  
US-09-949-016-10974  
Sequence 10974, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10974  
LENGTH: 313  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-10974

Query Match 11.7%; Score 131; DB 4; Length 313;  
Best Local Similarity 23.0%; Pred. No. 8.8e-06;  
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVSETEAVQGNPMKLCISCMKREVEAT--TVVEWYRPEGKDFL-IYEYRNGHQ 82  
DB 84 VYTPKEIFVANGOGKLTG---KFKSTSTGGLTSVMSFQEGADTVTSFHHYSGGV 139  
QY 83 EVES--PFOGRLOWNSKDLQDVSIYLVNTLNDGLYTCNVSRFEFEHRRPVKTRRL 140  
DB 140 YLGNYPFKRISWAGDLKKDASININEMQFIHNGTYICDVKN-----183  
QY 141 IPLRVTEAGEDFTSVSE-----IMMYILVFLTLLIEMIYC--YRK-----183  
DB 184 -PPDIVQPGHIRLYVEKENLPPFPVWVVGIVTAVVGLTLLISMLAVLYRRKNSKR 242  
QY 184 -----VSKAEBAQENASD---YLAIPSENKENSAY 211  
DB 243 DYTGCSTSESLSPVKAQPRKSPSDTEGLVKSLSFGSHQGPVI 284

RESULT 9  
US-09-430-503-44  
; Sequence 44, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-44

Query Match 11.5%; Score 129; DB 3; Length 199;  
Best Local Similarity 26.0%; Pred. No. 7.5e-06;  
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSETEAVQGNPMKLRICISCMKREBEVAT--TVWEMFYRPEGKDFL-IYERYNGHQ 82  
DB 40 VYTPKEIFVANGTQGLKTC---KFKSTSTTGLTSVSMSPQEGADTTVSFFHYSQGOV 95  
QY 83 EVES--PQGRLOMNGSKDLODVSITVAVTLNDSGLYTCNVSRFEFEAHRPVKTRRL 140  
DB 96 YLGNVPPFKDRISWAGDLDKDKDASINIEHQFIHNGTYICDVKN----- 139  
QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTMLLIMTYCY---RKVSKA 187  
DB 140 -PPDIVQPGHIRLYVEKENLPVFPVWVVGIVTAVVLGLTLLISMLAVLYRRKSKR 198  
QY 188 E 188  
DB 199 D 199

RESULT 10  
US-09-430-503-48  
; Sequence 48, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 48  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-48

Query Match 11.5%; Score 129; DB 3; Length 199;  
Best Local Similarity 26.0%; Pred. No. 7.5e-06;  
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSETEAVQGNPMKLRICISCMKREBEVAT--TVWEMFYRPEGKDFL-IYERYNGHQ 82  
DB 40 VYTPKEIFVANGTQGLKTC---KFKSTSTTGLTSVSMSPQEGADTTVSFFHYSQGOV 95  
QY 83 EVES--PQGRLOMNGSKDLODVSITVAVTLNDSGLYTCNVSRFEFEAHRPVKTRRL 140  
DB 96 YLGNVPPFKDRISWAGDLDKDKDASINIEHQFIHNGTYICDVKN----- 139

QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTMLLIMTYCY---RKVSKA 187  
DB 140 -PPDIVQPGHIRLYVEKENLPVFPVWVVGIVTAVVLGLTLLISMLAVLYRRKSKR 198  
QY 188 E 188  
DB 199 D 199

RESULT 11  
US-09-430-503-42  
; Sequence 42, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-42

Query Match 11.3%; Score 127; DB 3; Length 199;  
Best Local Similarity 26.0%; Pred. No. 1.2e-05;  
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSETEAVQGNPMKLRICISCMKREBEVAT--TVWEMFYRPEGKDFL-IYERYNGHQ 82  
DB 40 VYTPKEIFVANGTQGLKTC---KFKSTSTTGLTSVSMSPQEGADTTVSFFHYSQGOV 95  
QY 83 EVES--PQGRLOMNGSKDLODVSITVAVTLNDSGLYTCNVSRFEFEAHRPVKTRRL 140  
DB 96 YLGNVPPFKDRISWAGDLDKDKDASINIEHQFIHNGTYICDVKN----- 139  
QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTMLLIMTYCY---RKVSKA 187  
DB 140 -PPDIVQPGHIRLYVEKENLPVFPVWVVGIVTAVVLGLTLLISMLAVLYRRKSKR 198  
QY 188 E 188  
DB 199 D 199

RESULT 12  
US-09-430-503-46  
; Sequence 46, Application US/09430503  
; Patent No. 6355786  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Zhizhuang  
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND  
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME  
; CURRENT APPLICATION NUMBER: US/09/430,503  
; CURRENT FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-503-46

Query Match 11.3%; Score 127; DB 3; Length 199;  
Best Local Similarity 26.0%; Pred. No. 1.2e-05;  
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSETEAVQGNPMKLRICISCMKREBEVAT--TVWEMFYRPEGKDFL-IYERYNGHQ 82



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Db      40 VYTPKEIFVANGTQGLTCTC-----KFKSTSTTGGLTYSVMSFQPEGADTTVSFFHYSGQV 95
QY      83 EVES--PFGRLQWNGSKLDQVSTIVLVNTLNDGSLYTCNVSREFEFAHREFVKTTRL 140
Db      96 YLGNYPFPKDRISWAGDLDKDASININEMQFIHNGTYICDVKN-----139
QY      141 IPLRVTEAGDEPTSVSE-----IMMYILLVFLTMLIEMICY---RKVSKA 187
Db      140 -PPDIVVQGHIRLYVEKENLPPFPVWVVGIVTAVVLGLTLLISMLAVLYRRKNSKR 198
QY      188 E 188
Db      199 D 199

RESULT 13
US-09-430-503-18
; Sequence 18, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-18
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Query Match      11.3%; Score 127; DB 3; Length 209;
Best Local Similarity 26.0%; Pred. No. 1.3e-05;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;
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QY      27 VEVPSSETAVQGNPMKLRICISCKRREVEAT---TVWEFYPREGGKDFL-IYEYRNHQ 82
Db      40 VYTPKEIFVANGTQGLTCTC-----KFKSTSTTGGLTYSVMSFQPEGADTTVSFFHYSGQV 95
QY      83 EVES--PFGRLQWNGSKLDQVSTIVLVNTLNDGSLYTCNVSREFEFAHREFVKTTRL 140
Db      96 YLGNYPFPKDRISWAGDLDKDASININEMQFIHNGTYICDVKN-----139
QY      141 IPLRVTEAGDEPTSVSE-----IMMYILLVFLTMLIEMICY---RKVSKA 187
Db      140 -PPDIVVQGHIRLYVEKENLPPFPVWVVGIVTAVVLGLTLLISMLAVLYRRKNSKR 198
QY      188 E 188
Db      199 D 199

RESULT 14
US-09-430-503-20
; Sequence 20, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-430-503-20

Query Match 11.3%; Score 127; DB 3; Length 209;  
Best Local Similarity 26.0%; Pred. No. 1.3e-05;  
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

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QY      27 VEVPSSETAVQGNPMKLRICISCKRREVEAT---TVWEFYPREGGKDFL-IYEYRNHQ 82
Db      40 VYTPKEIFVANGTQGLTCTC-----KFKSTSTTGGLTYSVMSFQPEGADTTVSFFHYSGQV 95
QY      83 EVES--PFGRLQWNGSKLDQVSTIVLVNTLNDGSLYTCNVSREFEFAHREFVKTTRL 140
Db      96 YLGNYPFPKDRISWAGDLDKDASININEMQFIHNGTYICDVKN-----139
QY      141 IPLRVTEAGDEPTSVSE-----IMMYILLVFLTMLIEMICY---RKVSKA 187
Db      140 -PPDIVVQGHIRLYVEKENLPPFPVWVVGIVTAVVLGLTLLISMLAVLYRRKNSKR 198
QY      188 E 188
Db      199 D 199
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RESULT 15
US-09-430-503-22
; Sequence 22, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-22
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Query Match 11.3%; Score 127; DB 3; Length 209;  
Best Local Similarity 26.0%; Pred. No. 1.3e-05;  
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

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QY      27 VEVPSSETAVQGNPMKLRICISCKRREVEAT---TVWEFYPREGGKDFL-IYEYRNHQ 82
Db      40 VYTPKEIFVANGTQGLTCTC-----KFKSTSTTGGLTYSVMSFQPEGADTTVSFFHYSGQV 95
QY      83 EVES--PFGRLQWNGSKLDQVSTIVLVNTLNDGSLYTCNVSREFEFAHREFVKTTRL 140
Db      96 YLGNYPFPKDRISWAGDLDKDASININEMQFIHNGTYICDVKN-----139
QY      141 IPLRVTEAGDEPTSVSE-----IMMYILLVFLTMLIEMICY---RKVSKA 187
Db      140 -PPDIVVQGHIRLYVEKENLPPFPVWVVGIVTAVVLGLTLLISMLAVLYRRKNSKR 198
QY      188 E 188
Db      199 D 199
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Job time : 30 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:21:59 ; Search time 91.5 Seconds  
(without alignments)  
779.153 Million cell updates/sec

Title: US-09-977-579-2

Perfect score: 1124  
Sequence: 1 MPAENRFLPLASLVLYWVS.....SDYLAIPEKENSAPVVE 215

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Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:\*

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- 3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*
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- 8: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*
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- 10: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 12: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 17: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	215	11	US-09-977-579-2
2	1124	100.0	215	14	US-10-142-201B-11
3	1105	98.3	215	11	US-09-977-579-1
4	1105	98.3	215	13	US-10-029-191-2
5	1105	98.3	215	14	US-10-142-201B-12
6	986	87.7	191	13	US-10-029-191-4
7	983	75.0	159	11	US-09-977-579-22
8	832	74.0	159	11	US-09-977-579-23
9	597	53.1	111	13	US-10-029-191-5
10	477	42.4	218	13	US-10-029-191-20
11	472	42.0	218	11	US-09-977-579-44
12	471	41.9	218	14	US-10-142-201B-8
13	471	41.9	218	16	US-10-477-272-2

14	282	25.1	58	13	US-10-029-191-7	Sequence 7, App1
15	258.5	23.0	268	15	US-09-875-456A-14	Sequence 14, App1
16	258.5	23.0	268	15	US-10-401-915-14	Sequence 14, App1
17	234	20.8	74	15	US-10-276-774-2068	Sequence 2068, App
18	207	18.4	39	11	US-09-977-579-17	Sequence 17, App1
19	196	17.4	39	11	US-09-977-579-18	Sequence 18, App1
20	167	14.9	248	15	US-10-205-531-110	Sequence 110, App
21	165	14.7	34	11	US-09-977-579-31	Sequence 31, App1
22	163.5	14.5	248	15	US-10-016-248-54	Sequence 54, App1
23	163.5	14.5	251	15	US-10-016-248-52	Sequence 52, App1
24	163.5	14.5	258	15	US-10-016-248-53	Sequence 53, App1
25	161	14.3	34	11	US-09-977-579-47	Sequence 47, App1
26	160.5	14.3	235	13	US-10-053-107-12	Sequence 12, App1
27	160.5	14.3	235	14	US-10-227-884-238	Sequence 238, App
28	160.5	14.3	235	14	US-10-230-163-238	Sequence 238, App
29	160.5	14.3	235	14	US-10-230-338-238	Sequence 238, App
30	160.5	14.3	235	14	US-10-218-631-238	Sequence 238, App
31	160.5	14.3	235	14	US-10-230-414-238	Sequence 238, App
32	160.5	14.3	235	14	US-10-213-145-12	Sequence 12, App1
33	160.5	14.3	235	14	US-10-232-224-238	Sequence 238, App
34	160.5	14.3	235	14	US-10-216-158A-238	Sequence 238, App
35	160.5	14.3	235	14	US-10-218-848-238	Sequence 238, App
36	160.5	14.3	235	14	US-10-227-873-238	Sequence 238, App
37	160.5	14.3	235	14	US-10-227-883-238	Sequence 238, App
38	160.5	14.3	235	14	US-10-219-076-238	Sequence 238, App
39	160.5	14.3	235	14	US-10-230-434-238	Sequence 238, App
40	160.5	14.3	235	14	US-10-213-199-12	Sequence 12, App1
41	160.5	14.3	235	14	US-10-219-003-238	Sequence 238, App
42	160.5	14.3	235	14	US-10-219-075-238	Sequence 238, App
43	160.5	14.3	235	14	US-10-219-464-238	Sequence 238, App
44	160.5	14.3	235	14	US-10-219-466-238	Sequence 238, App
45	160.5	14.3	235	14	US-10-219-479-238	Sequence 238, App

#### ALIGNMENTS

RESULT 1  
US-09-977-579-2  
Sequence 2, Application US/09977579  
Publication No. US20040248240A1  
GENERAL INFORMATION:  
APPLICANT: Cambridge University Technical Services  
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi  
TITLE OF INVENTION: Channel  
FILE REFERENCE: 674558-2001  
CURRENT APPLICATION NUMBER: US/09/977, 579  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: PCT/EP00/01783  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60,129,473  
PRIOR FILING DATE: 2000-02-24  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 215  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-977-579-2

Query Match 100.0%; Score 1124; DB 11; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.9e+104;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPAENRFLPLASLVLYWVSVCPCVSEVSEFBAVQGNPMKURICSCMKREBEATTVV 60  
DB 1 MPAENRFLPLASLVLYWVSVCPCVSEVSEFBAVQGNPMKURICSCMKREBEATTVV 60  
QY 61 EWFYREGGKDFLIYRYNGHGVESPPQGRLOQWNSKDLQDVSTVLVNTLNDGLYTC 120  
DB 61 EWFYREGGKDFLIYRYNGHGVESPPQGRLOQWNSKDLQDVSTVLVNTLNDGLYTC 120

QY 121 NVSRFEFEARHPFKTTRLPLRVTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
DB 121 NVSRFEFEARHPFKTTRLPLRVTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
QY 181 YRKVSKAEBAQAENASDYLAIPSENKENSAPVVEE 215  
DB 181 YRKVSKAEBAQAENASDYLAIPSENKENSAPVVEE 215

## RESULT 2

US-10-142-201B-11  
; Sequence 11, Application US/10142201B  
; Publication No. US20030022205A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; APPLICANT: Curtis, Rory A.J. SODIUM CHANNEL BETA 4 SUBUNIT,  
; TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MP12001-106P1RN (M)  
; CURRENT APPLICATION NUMBER: US/10/142,201B  
; PRIOR FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: US 60/289,893  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-142-201B-11

Query Match 100.0%; Score 1124; DB 14; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.9e-104;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYVWVCFVPCVSEVPSSETEAQGNPMKLRICISCMKREBEVATTIV 60  
DB 1 MPAFNRLLPLASLVLIYVWVCFVPCVSEVPSSETEAQGNPMKLRICISCMKREBEVATTIV 60  
QY 61 EMFYRPEGKDFLIYERNNGHGVESPPQGRLONNGSKDLODVSTIVLVNTLNDGGLTYC 120  
DB 61 EMFYRPEGKDFLIYERNNGHGVESPPQGRLONNGSKDLODVSTIVLVNTLNDGGLTYC 120  
QY 121 NVSRFEFEARHPFKTTRLPLRVTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
DB 121 NVSRFEFEARHPFKTTRLPLRVTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
QY 181 YRKVSKAEBAQAENASDYLAIPSENKENSAPVVEE 215  
DB 181 YRKVSKAEBAQAENASDYLAIPSENKENSAPVVEE 215

## RESULT 3

US-09-977-579-1  
; Sequence 1, Application US/09977579  
; Publication No. US20040248240A1  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge University Technical Services  
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod  
; TITLE OF INVENTION: Channel  
; FILE REFERENCE: 674558-2001  
; CURRENT APPLICATION NUMBER: US/09/977,579  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP00/01783  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60,129,473  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 215  
; TYPE: PRT

; ORGANISM: Rat  
US-09-977-579-1

Query Match 98.3%; Score 1105; DB 11; Length 215;  
Best Local Similarity 98.1%; Pred. No. 1.5e-102;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYVWVCFVPCVSEVPSSETEAQGNPMKLRICISCMKREBEVATTIV 60  
DB 1 MPAFNRLLPLASLVLIYVWVCFVPCVSEVPSSETEAQGNPMKLRICISCMKREBEVATTIV 60  
QY 61 EMFYRPEGKDFLIYERNNGHGVESPPQGRLONNGSKDLODVSTIVLVNTLNDGGLTYC 120  
DB 61 EMFYRPEGKDFLIYERNNGHGVESPPQGRLONNGSKDLODVSTIVLVNTLNDGGLTYC 120  
QY 121 NVSRFEFEARHPFKTTRLPLRVTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
DB 121 NVSRFEFEARHPFKTTRLPLRVTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
QY 181 YRKVSKAEBAQAENASDYLAIPSENKENSAPVVEE 215  
DB 181 YRKVSKAEBAQAENASDYLAIPSENKENSAPVVEE 215

## RESULT 4

US-10-029-191-2  
; Sequence 2, Application US/10029191  
; Publication No. US20020160453A1  
; GENERAL INFORMATION:  
; APPLICANT: CURTIS, RORY A.J.  
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
; FILE REFERENCE: 210147.00XX/5U1  
; CURRENT APPLICATION NUMBER: US/10/029,191  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/569,978  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/134,198  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-029-191-2

Query Match 98.3%; Score 1105; DB 13; Length 215;  
Best Local Similarity 98.1%; Pred. No. 1.5e-102;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYVWVCFVPCVSEVPSSETEAQGNPMKLRICISCMKREBEVATTIV 60  
DB 1 MPAFNRLLPLASLVLIYVWVCFVPCVSEVPSSETEAQGNPMKLRICISCMKREBEVATTIV 60  
QY 61 EMFYRPEGKDFLIYERNNGHGVESPPQGRLONNGSKDLODVSTIVLVNTLNDGGLTYC 120  
DB 61 EMFYRPEGKDFLIYERNNGHGVESPPQGRLONNGSKDLODVSTIVLVNTLNDGGLTYC 120  
QY 121 NVSRFEFEARHPFKTTRLPLRVTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
DB 121 NVSRFEFEARHPFKTTRLPLRVTEBAGDEFTSVSEIMMYILLVFLTMLIEMTYC 180  
QY 181 YRKVSKAEBAQAENASDYLAIPSENKENSAPVVEE 215  
DB 181 YRKVSKAEBAQAENASDYLAIPSENKENSAPVVEE 215

## RESULT 5

US-10-142-201B-12  
; Sequence 12, Application US/10142201B  
; Publication No. US20030022205A1  
; GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals Inc.  
APPLICANT: Curtis, Rory A.J.  
TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT.  
TITLE OF INVENTION: AND USES THEREFOR  
FILE REFERENCE: MPI2001-106P(RN/IM)  
CURRENT APPLICATION NUMBER: US/10/142,2018  
CURRENT FILING DATE: 2002-05-09  
PRIOR APPLICATION NUMBER: US 60/289,893  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 215  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-10-142-2018-12

Query Match 98.3%; Score 1105; DB 14; Length 215;  
Best Local Similarity 98.1%; Pred. No. 1.5e-102;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPANRLPLASLVLIIWVSVCPPVCEVSETEAVOGNPKLKRCISCMKREVEATTVV 60  
DB 1 MPANRLPLASLVLIIWVSVCPPVCEVSETEAVOGNPKLKRCISCMKREVEATTVV 60  
QY 61 EMFRRPGKDFLIYERNGHOEVSPFOGRLQNGSKDLODVSIITVLTNTLNDGSLGTYC 120  
DB 61 EMFRRPGKDFLIYERNGHOEVSPFOGRLQNGSKDLODVSIITVLTNTLNDGSLGTYC 120  
QY 121 NVSREFFEAHRPFPVKTTRLIPRVTEAGEDEFTSVSEIMMYLIVFLTLMLEIMIYC 180  
DB 121 NVSREFFEAHRPFPVKTTRLIPRVTEAGEDEFTSVSEIMMYLIVFLTLMLEIMIYC 180  
QY 181 YRKVSKAEBAOENASDYLAIPSENKENSAPVVEE 215  
DB 181 YRKVSKAEBAOENASDYLAIPSENKENSAPVVEE 215

RESULT 6  
US-10-029-191-4  
Sequence 4, Application US/10029191  
Publication No. US20020160453A1  
GENERAL INFORMATION:  
APPLICANT: CURTIS, RORY A.J.  
TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
FILE REFERENCE: 210147.00XX/501  
CURRENT APPLICATION NUMBER: US/10/029,191  
CURRENT FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 09/569,978  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/134,198  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 191  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-10-029-191-4

Query Match 87.7%; Score 986; DB 13; Length 191;  
Best Local Similarity 99.0%; Pred. No. 1.2e-90;  
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 VCVEVSETEAVOGNPKLKRCISCMKREVEATTVVEMFRRPGKDFLIYERNGHOEV 84  
DB 1 VCVEVSETEAVOGNPKLKRCISCMKREVEATTVVEMFRRPGKDFLIYERNGHOEV 60  
QY 85 ESPFOGRLQNGSKDLODVSIITVLTNTLNDGSLGTYCNSREFFEAHRPFPVKTTRLIPLR 144  
DB 61 ESPFOGRLQNGSKDLODVSIITVLTNTLNDGSLGTYCNSREFFEAHRPFPVKTTRLIPLR 120

QY 145 VTEAGEDEFTSVSEIMMYLIVFLTLMLEIMIYCYRKVSKAEBAOENASDYLAIPSE 204  
DB 121 VTEAGEDEFTSVSEIMMYLIVFLTLMLEIMIYCYRKVSKAEBAOENASDYLAIPSE 180  
QY 205 NKENSAPVVEE 215  
DB 181 NKENSAPVVEE 191

RESULT 7  
US-09-977-579-22

Sequence 22, Application US/09977579  
Publication No. US20040248240A1  
GENERAL INFORMATION:  
APPLICANT: Cambridge University Technical Services  
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod  
TITLE OF INVENTION: channel  
FILE REFERENCE: 674558-2001  
CURRENT APPLICATION NUMBER: US/09/977,579  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: PCT/EP00/01783  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60,129,473  
PRIOR FILING DATE: 2000-02-24  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 159  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-977-579-22

Query Match 75.0%; Score 843; DB 11; Length 159;  
Best Local Similarity 100.0%; Pred. No. 2e-76;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANRLPLASLVLIIWVSVCPPVCEVSETEAVOGNPKLKRCISCMKREVEATTVV 60  
DB 1 MPANRLPLASLVLIIWVSVCPPVCEVSETEAVOGNPKLKRCISCMKREVEATTVV 60  
QY 61 EMFRRPGKDFLIYERNGHOEVSPFOGRLQNGSKDLODVSIITVLTNTLNDGSLGTYC 120  
DB 61 EMFRRPGKDFLIYERNGHOEVSPFOGRLQNGSKDLODVSIITVLTNTLNDGSLGTYC 120  
QY 121 NVSREFFEAHRPFPVKTTRLIPRVTEAGEDEFTSVSE 159  
DB 121 NVSREFFEAHRPFPVKTTRLIPRVTEAGEDEFTSVSE 159

RESULT 8  
US-09-977-579-23

Sequence 23, Application US/09977579  
Publication No. US20040248240A1  
GENERAL INFORMATION:  
APPLICANT: Cambridge University Technical Services  
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod  
TITLE OF INVENTION: channel  
FILE REFERENCE: 674558-2001  
CURRENT APPLICATION NUMBER: US/09/977,579  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: PCT/EP00/01783  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60,129,473  
PRIOR FILING DATE: 2000-02-24  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 23  
LENGTH: 159  
TYPE: PRT  
ORGANISM: Rat  
US-09-977-579-23

Query Match 74.0%; Score 832; DB 11; Length 159;  
Best Local Similarity 98.7%; Pred. No. 2.6e-75;  
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAFNRPLPLALVLIYWSVCPVCEVPEVSETEAVQGNPMKLRCTSCMKREVEATTVV 60  
DB 1 MAFNRPLPLALVLIYWSVCPVCEVPEVSETEAVQGNPMKLRCTSCMKREVEATTVV 60  
QY 61 EHFYRPEGKDFLIYERNGHOVESPFQGRLOMNGSKDLODVSTIVLNTLNDGSLYTC 120  
DB 61 EHFYRPEGKDFLIYERNGHOVESPFQGRLOMNGSKDLODVSTIVLNTLNDGSLYTC 120  
QY 121 NVSRFEFEARHPFVKTRRLPLRVTGEAGDEFTSVSE 159  
DB 121 NVSRFEFEARHPFVKTRRLPLRVTGEAGDEFTSVSE 159

## RESULT 9

US-10-029-191-5  
; Sequence 5, Application US/10029191  
; Publication No. US20020160453A1  
; GENERAL INFORMATION:  
; APPLICANT: CURTIS, ROY A.J.  
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
; FILE REFERENCE: 210147.00XX/5U1  
; CURRENT APPLICATION NUMBER: US/10/029,191  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/569,978  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/134,198  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-029-191-5

Query Match 53.1%; Score 597; DB 13; Length 111;  
Best Local Similarity 100.0%; Pred. No. 6.3e-52;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 VCEVPSSETEAVQGNPMKLRCTSCMKREVEATTVVEMFYRPEGKDFLIYERNGHOEV 84  
DB 1 VCEVPSSETEAVQGNPMKLRCTSCMKREVEATTVVEMFYRPEGKDFLIYERNGHOEV 60  
QY 85 ESPFGRLQMGSKDLODVSTIVLNTLNDGSLYTCNVSREFEFAHRFPV 135  
DB 61 ESPFGRLQMGSKDLODVSTIVLNTLNDGSLYTCNVSREFEFAHRFPV 111

## RESULT 10

US-10-029-191-20  
; Sequence 20, Application US/10029191  
; Publication No. US20020160453A1  
; GENERAL INFORMATION:  
; APPLICANT: CURTIS, ROY A.J.  
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
; FILE REFERENCE: 210147.00XX/5U1  
; CURRENT APPLICATION NUMBER: US/10/029,191  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/569,978  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/134,198  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 218

TYPE: PRT  
ORGANISM: Lepus Sp.  
US-10-029-191-20

Query Match 42.4%; Score 477; DB 13; Length 218;  
Best Local Similarity 49.5%; Pred. No. 1.7e-39;  
Matches 106; Conservative 32; Mismatches 66; Indels 8; Gaps 5;

QY 10 LASLVLIYWSVCPVCEVPEVSETEAVQGNPMKLRCTSCMKREVEATTVVEMFYRPEG 69  
DB 5 LAFVGAALVSSAWGCVPEVSETEAVYGMFKLICISCKRSETTAFTFEMTRQGT 64  
QY 70 KDPL-IYERNGHOVESPF--FQGRLOMNGS---KDLQDVSTIVLNTLNDGSLYTCNV 123  
DB 65 BEFKILRYENEVLQLEDERFERGVRVWNGSRGTQDLOLSIFITNVYNNHSGDYCHY 124  
QY 124 REFEEARHPFVKTRRLPLRVTGEAGDEFTSVSEIMMYILVLTMLIEMTYCYRK 183  
DB 125 RLSPFENYENHTSVVKKIHLEVDQANDMASIVSEIMMYILVLTMLVLAEMVYCYRK 184  
QY 184 VSKA-EBAAGENASDYLAIPSENKEN-SAPVEE 215  
DB 185 IAAATEAAAGENASEYLAITSESKENCYGVAAE 218

## RESULT 11

US-09-977-579-44  
; Sequence 44, Application US/09977579  
; Publication No. US20040240240A1  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge University Technical Services  
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi  
; TITLE OF INVENTION: channel  
; FILE REFERENCE: 674558-2001  
; CURRENT APPLICATION NUMBER: US/09/977,579  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP00/01783  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60,129,473  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 44  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-977-579-44

Query Match 42.0%; Score 472; DB 11; Length 218;  
Best Local Similarity 49.1%; Pred. No. 5.4e-39;  
Matches 105; Conservative 33; Mismatches 68; Indels 8; Gaps 5;

QY 10 LASLVLIYWSVCPVCEVPEVSETEAVQGNPMKLRCTSCMKREVEATTVVEMFYRPEG 69  
DB 5 LALVGAALVSSAWGCVPEVSETEAVYGMFKLICISCKRSETTAFTFEMTRQGT 64  
QY 70 KDPL-IYERNGHOVESPF--FQGRLOMNGS---KDLQDVSTIVLNTLNDGSLYTCNV 123  
DB 65 BEFKILRYENEVLQLEDERFERGVRVWNGSRGTQDLOLSIFITNVYNNHSGDYCHY 124  
QY 124 REFEEARHPFVKTRRLPLRVTGEAGDEFTSVSEIMMYILVLTMLIEMTYCYRK 183  
DB 125 RLSPFENYENHTSVVKKIHLEVDQANDMASIVSEIMMYILVLTMLVLAEMVYCYRK 184  
QY 184 VSKA-EBAAGENASDYLAIPSENKEN-SAPVEE 215  
DB 185 IAAATEAAAGENASEYLAITSESKENCYGVAAE 218

## RESULT 12

US-10-142-201B-8  
; Sequence 8, Application US/10142201B

Publication No. US20030022205A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals Inc.  
APPLICANT: Curtis, Rory A.J.  
TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,  
TITLE OF INVENTION: AND USES THEREFOR  
FILE REFERENCE: MPI2001-106P1RN(M)  
CURRENT APPLICATION NUMBER: US/10/142,201B  
CURRENT FILING DATE: 2002-05-09  
PRIORITY APPLICATION NUMBER: US 60/289,893  
PRIORITY FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-142-201B-8

Query Match 41.9%; Score 471; DB 14; Length 218;  
Best Local Similarity 49.5%; Pred. No. 6.8e-39;  
Matches 106; Conservative 31; Mismatches 69; Indels 8; Gaps 5;

QY 10 LASLVLIVWVSCFPCVEVPSETEAVQGNPMKLRCSCKMREBEVATTVVEWFRPEG 69  
DB 5 LALVVGALVSSACGCGVEVDSETEAVYGMTFKILCSCKRSETNAETFTWTFROKGT 64  
QY 70 KDFL-IEYVNGHQEVSP--FOGRLQWNGS--KDLQVSIIVLNTLNDGSLYTCNV 123  
DB 65 EEEFKILRYENEVLQLEDEDRFEGRVVWNGSRGTQDLQDLSIFITVNTYVHSGDYECV 124  
QY 124 REEFEEAHRPFVKTTRLIPRLVTEAGEDEFTSVSEIMMYLLVFLTLMLLIEMICYRK 183  
DB 125 RLFFENYEHNTSVVKKIHIEVDKANDVASIYSEIMMYLLVFLTLMLLIEMICYRK 184  
QY 184 VSKA-EBAQENASDYLAIPSENKEN-SAYPVEE 215  
DB 185 IAAETFAQENASEYLAITSSEKENCCTGVQVAE 218

RESULT 13  
US-10-477-272-2  
Sequence 2, Application US/10477272  
Publication No. US20040191791A1  
GENERAL INFORMATION:  
APPLICANT: Biomedics Limited  
TITLE OF INVENTION: P12  
FILE REFERENCE: SCN1B (R85C)  
CURRENT APPLICATION NUMBER: US/10/477,272  
CURRENT FILING DATE: 2003-11-10  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-477-272-2

Query Match 41.9%; Score 471; DB 16; Length 218;  
Best Local Similarity 49.5%; Pred. No. 6.8e-39;  
Matches 106; Conservative 31; Mismatches 69; Indels 8; Gaps 5;

QY 10 LASLVLIVWVSCFPCVEVPSETEAVQGNPMKLRCSCKMREBEVATTVVEWFRPEG 69  
DB 5 LALVVGALVSSACGCGVEVDSETEAVYGMTFKILCSCKRSETNAETFTWTFROKGT 64  
QY 70 KDFL-IEYVNGHQEVSP--FOGRLQWNGS--KDLQVSIIVLNTLNDGSLYTCNV 123  
DB 65 EEEFKILRYENEVLQLEDEDRFEGRVVWNGSRGTQDLQDLSIFITVNTYVHSGDYECV 124  
QY 124 REEFEEAHRPFVKTTRLIPRLVTEAGEDEFTSVSEIMMYLLVFLTLMLLIEMICYRK 183  
DB 125 RLFFENYEHNTSVVKKIHIEVDKANDVASIYSEIMMYLLVFLTLMLLIEMICYRK 184

QY 184 VSKA-EBAQENASDYLAIPSENKEN-SAYPVEE 215  
DB 185 IAAETFAQENASEYLAITSSEKENCCTGVQVAE 218

RESULT 14  
US-10-029-191-7  
Sequence 7, Application US/10029191  
Publication No. US20020160453A1  
GENERAL INFORMATION:  
APPLICANT: CURTIS, RORY A.J.  
TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT  
FILE REFERENCE: 210147.00XX/501  
CURRENT APPLICATION NUMBER: US/10/029,191  
CURRENT FILING DATE: 2001-12-20  
PRIORITY APPLICATION NUMBER: 09/569,978  
PRIORITY FILING DATE: 2000-05-12  
PRIORITY APPLICATION NUMBER: US 60/134,198  
PRIORITY FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-10-029-191-7

Query Match 25.1%; Score 282; DB 13; Length 58;  
Best Local Similarity 96.6%; Pred. No. 1.1e-20;  
Matches 56; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 158 SEIMMYLLVFLTLMLLIEMICYRKVSKAEBAQENASDYLAIPSENKENSAYPVEE 215  
DB 1 SEIMMYLLVFLTLMLLIEMICYRKVSKAEBAQENASDYLAIPSENKENSAYPVEE 58

RESULT 15  
US-09-875-456A-14  
Sequence 14, Application US/09875456A  
Patent No. US20020045229A1  
GENERAL INFORMATION:  
APPLICANT: Qin, Ming  
APPLICANT: Codd, Ellen  
TITLE OF INVENTION: DNAs encoding human beta1 sodium channel subunit  
FILE REFERENCE: ORT-1221  
CURRENT APPLICATION NUMBER: US/09/875,456A  
CURRENT FILING DATE: 2001-09-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 268  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-875-456A-14

Query Match 23.0%; Score 258.5; DB 9; Length 268;  
Best Local Similarity 43.2%; Pred. No. 1.9e-17;  
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 10 LASLVLIVWVSCFPCVEVPSETEAVQGNPMKLRCSCKMREBEVATTVVEWFRPEG 69  
DB 5 LALVVGALVSSACGCGVEVDSETEAVYGMTFKILCSCKRSETNAETFTWTFROKGT 64  
QY 70 KDFL-IEYVNGHQEVSP--FOGRLQWNGS--KDLQVSIIVLNTLNDGSLYTCNV 123  
DB 65 EEEFKILRYENEVLQLEDEDRFEGRVVWNGSRGTQDLQDLSIFITVNTYVHSGDYECV 124  
QY 124 REEFEEAHRPFVKTTRLIPRLVTEAGE 151  
DB 125 RLFFENYEHNTSVVKKIHIEVDK-GE 151

Search completed: March 31, 2005, 20:39:33  
Job time : 92.5 secs

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C:Superfamily: myelin P0 protein; immunoglobulin homology  
 C:Keywords: glycoprotein; membrane protein; myelin; phosphoprotein; Schwann cell; struct  
 F:14-100/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 159; DB 1; Length 219;  
 Best Local Similarity 26.5%; Pred. No. 2.2e-06;  
 Matches 52; Conservative 31; Mismatches 99; Indels 14; Gaps 6;

25 VCEVPSEAEVAQGNPKLRCTSCMKREBEATVWEMYPEEGKDFL-ITYEYRNGQVE 83  
 1 IYVYDKEVHGAVGSQVTLTYC-SFWSSEWSDLSFTWRIOPEGGRDAISIFHAKGQPY 59  
 84 VE--SPFOGRLQWNGSKLDQVSTIVLNTLNDGLYTCNVSREFEFARPPVKTTRLI 141  
 60 IDEVGTFFKRIQWGDPRHKDGSIVIHNLVDYDNGFTCDVANNPD-----IVGKTQGV 113  
 142 PLRVTEAGDEFTSVSEIMMTILVFLTMLLMI-YCYRKVSKAEBA--AQENASD 197  
 114 TLVEEKPTRRYGVVIGAVLGVLALLFLYIRCYMLRQAAALQRLHAMEKGL 173  
 DB VLAISENKENASAVPV 213  
 174 HKTAKDASKRGKQTPV 189

## RESULT 8

A54662  
 myelin P0 protein - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jan-2000  
 C:Accession: A54662

R:You, K.H.; Hsieh, C.L.; Hayes, C.; Stahl, N.; Francke, U.; Popko, B.  
 Genomics 9, 751-757, 1991

A:Title: DNA sequence, genomic organization, and chromosomal localization of the mouse P  
 A:Reference number: A54662; MUID:91244320; PMID:1709914

A:Status: preliminary  
 A:Accession: A54662  
 A:Molecule type: DNA

A:Residues: 1-247 <YOU>  
 A:Cross-references: GB:M62427  
 C:Superfamily: myelin P0 protein; immunoglobulin homology  
 F:43-128/Domain: immunoglobulin homology <IMM>

Query Match 13.7%; Score 154.5; DB 1; Length 247;  
 Best Local Similarity 27.6%; Pred. No. 6e-06;  
 Matches 58; Conservative 34; Mismatches 99; Indels 19; Gaps 8;

11 ASLVLIYVSVCFVCEVPSEAEVAQGNPKLRCTSCMKREBEATVWEMYPEEGK 70  
 20 SSVLV-----SPALAIYVYTDREITGVAGVGSQVTLHC-SFWSSEWSDLSFTWRIO-EGGR 73  
 71 DFL-ITYEYRNGQVE--SPFOGRLQWNGSKLDQVSTIVLNTLNDGLYTCNVSREFE 127  
 74 DAISIFHAKGQPYIDEGVAFKRIQWGDPRMKDGSIVIHNLVDYSDNGFTCDVANNPD 133  
 128 FEARHPVKTTRLIPLRVTEAGDEFTSVSEIMMTILVFLTMLLMI-YCYRKVSK 186  
 134 -----IVGKTQGVTLTYVEKVPTRRYGVVIGAVLGVLALLFLYIRCYMLRQA 187  
 QY 187 AEE---AQENASDYLAIPSENKENASAVPV 213  
 DB 188 ALQRLHAMEKGRFHKSQDSKSRGQTPV 217

## RESULT 9

A52999  
 myelin P0 protein precursor - horn shark

C:Species: Heterodontus francisci (horn shark)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: A52999

R:Saavedra, R.A.; Fors, L.; Aebertold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood,  
 J. Mol. Evol. 29, 149-156, 1989

A:Title: The myelin proteins of the shark brain are similar to the myelin proteins of th

A:Reference number: A52999; MUID:90040744; PMID:2478717

A:Accession: A52999  
 A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-246 <SA>  
 A:Cross-references: UNIPROT:P20938; GB:X16714; NID:963976; PIDN:CA837865.1; PID:94467434  
 C:Superfamily: myelin P0 protein; immunoglobulin homology  
 C:Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein  
 F:41-127/Domain: immunoglobulin homology <IMM>

Query Match 12.9%; Score 144.5; DB 1; Length 246;  
 Best Local Similarity 25.8%; Pred. No. 4.3e-05;  
 Matches 49; Conservative 37; Mismatches 77; Indels 27; Gaps 7;

16 IYVWVCPVCEVPSEAEVAQGNPKLRCTSCMKREBEATVWEMYPEFP 66  
 10 LFCSVLVAFSVLRSGSISVTHNLHKTGSDVTLTYC-GFWSSEYSDLTLSMRFRP 68  
 67 EGKDFL-ITYEYRNGQVE--SPFOGRLQWNGSKLDQVSTIVLNTLNDGLYTCNVS 123  
 69 DNSRDIISIFHYGNGVPIEKMGQGRGVWGDISKDGSIVIRNLDYINDGFTCDVK 128  
 QY 124 REFEARHPVKTTRLIPLRVTEAGDEFTSVSEIMMTILVFLTMLLMI 178  
 DB 129 NPPD-----VVGTSDDVHLTYDKIPPVGAGVSGALITGFIILLVGLYL--FR 179  
 QY 179 CYRKVSKAE 188  
 DB 180 YVRRRANSE 189

## RESULT 10

A61087  
 myelin P0 glycoprotein precursor - chicken

C:Species: Gallus gallus (chicken)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: A61087

R:Barbu, M.  
 J. Neurosci. Res. 25, 143-151, 1990

A:Title: Molecular cloning of cDNAs that encode the chicken P0 protein: evidence for earl  
 A:Reference number: A61087; MUID:90204597; PMID:1690817

A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-249 <BAR>

A:Cross-references: UNIPROT:P37301  
 C:Comment: This protein is found only in peripheral nervous system Schwann cells.  
 C:Superfamily: myelin P0 protein; immunoglobulin homology  
 C:Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-249/Product: myelin P0 glycoprotein #status predicted <EXT>  
 F:30-153/Domain: extracellular #status predicted <EXT>  
 F:43-129/Domain: immunoglobulin homology <IMM>  
 F:154-179/Domain: transmembrane #status predicted <TM>  
 F:180-249/Domain: intracellular #status predicted <INT>  
 F:122/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 12.5%; Score 140.5; DB 1; Length 249;  
 Best Local Similarity 23.6%; Pred. No. 9.7e-05;  
 Matches 48; Conservative 43; Mismatches 87; Indels 25; Gaps 8;

13 IVLIVWVCFP-----VCEVPSEAEVAQGNPKLRCTSCMKREBEATVWEMYPEFP 67  
 13 LLVGLLSASGSPFLAHVYTPREVYGVTSHTLSC-SFWSSEWSEDSISYTHPFAE 71  
 68 GKKDFL-ITYEYRNGQVE--SPFOGRLQWNGSKLDQVSTIVLNTLNDGLYTCNVS 124  
 72 GSRDLSIFHYGKQGPYIDVGSEFKERMEWGNPRRKDGSIVIHNLVDYDNGFTCDVK 131  
 QY 125 EFEPARHPVKTTRLIPLRVTEAGDEFTSVSEIMMTILVFLTMLLMI-YCY-- 181  
 DB 132 PPD-----IVGKSQVTLTYVEKVPTRRYGVVIGAVLGVLALLVAVVAVVLRFCWLR 185

Qy 182 -----RKVSKAEAA-AQENASD 197  
 Db 186 ROAVLQRLRLSAMKGLQRSKD 208

## RESULT 11

A57843  
 sodium channel beta 2 subunit - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C/Accession: A57843  
 R/Isom: L.L.; Ragsdale, D.S.; DeJongh, K.S.; Westenhoeek, R.E.; Reber, B.F.X.; Scheuer, Cell 83, 433-442, 1995  
 A/Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transmembrane Protein  
 A/Reference number: A57843; PMID:96067641; PMID:8521473  
 A/Accession: A57843  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-215 <RES>  
 A/Cross-references: UNIPROT:P54900; EMBL:U37026; NID:91086496; PIDN:AAC52967.1; PID:91086496  
 C/Genetics: SCNB2

Query Match 10.5%; Score 118; DB 2; Length 215;  
 Best Local Similarity 25.1%; Pred. No. 0.007;  
 Matches 49; Conservative 41; Mismatches 85; Indels 20; Gaps 8;

Qy 27 VEVPSSTEAQGNPMKRLCT--SCMKREVEATVWEPYRPGG--KDFLYEYRNGH 81  
 Db 32 VLVPTLLSVLNGSDTRLPCTFNSCYTVNHKQFS--LNMWYQECSCNCEWFLQFRMKIN 89  
 Qy 82 QEVSPFOGLONGSKDLDVSTVLTNTLNDGLTCNVSRFEFEARPPVKTTRL 141  
 Db 90 LKIER-FGDKVERSGNPSKYDVSLTKNQLDEGICYITN--PPDRHGHGK---I 142  
 Qy 142 PLRVTEAGEDFTSVSEIMMYILVFLTLMLEIMY-CYRKVSKAEAAQENASDYL 200  
 Db 143 YLVQVLEVPERRSTVAIVIGASVGLAVIILVMVKVR-----KEQKLTSTDLDK 197  
 Qy 201 IPSENKENSAPVEE 215  
 Db 198 TEEBCKTDEGNAED 212

## RESULT 12

161783  
 sodium channel beta 2 subunit - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
 C/Accession: I61783  
 R/Isom: L.L.; Ragsdale, D.S.; DeJongh, K.S.; Westenhoeek, R.E.; Reber, B.F.X.; Scheuer, Cell 83, 433-442, 1995  
 A/Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transmembrane Protein  
 A/Reference number: A57843; PMID:96067641; PMID:8521473  
 A/Accession: I61783  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-186 <RES>  
 A/Cross-references: UNIPROT:Q62861; EMBL:U37147; NID:91086496; PIDN:AAB60506.1; PID:91086496  
 C/Genetics: SCNB2  
 A/Introns: 50/3; 120/2

Query Match 10.4%; Score 117; DB 2; Length 186;  
 Best Local Similarity 24.0%; Pred. No. 0.0073;  
 Matches 49; Conservative 38; Mismatches 79; Indels 38; Gaps 8;

Qy 27 VEVPSSTEAQGNPMKRLCT--SCMKREVEATVWEPYRPGGKDFLYEYRNGH 84  
 Db 3 VLVPTLLSVLNGSDTRLPCTFNSCYTVNHKQFS--LNMWYQ-----ECSCNCEW 50  
 Qy 85 ESPFO-----GRLOWGSKDLDVSTVLTNTLNDGLTCNVSRFEFEARH 132

Db 51 VLQFRMKIINTKLBERGDRVPSGNPSKYDVSTLKNVQLDEGICYITN--PPDRHR 108  
 Qy 133 PFVKTTRLPLRTEAGEDFTSVSEIMMYILVFLTLMLEIMY-CYRKVSKAEAA 191  
 Db 109 GHGK---YLVQVLEVPERRSTVAIVIGASVGLAVIILVMVKVR-----KKE 159  
 Qy 192 QENASDYLAIPSENKENSAPVEE 215  
 Db 160 QKLTSTDLDKTEEBCKTDEGNAED 183

## RESULT 13

S17295  
 fibroblast growth factor receptor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S17295  
 R/Raz, V.; Kojima, Z.; Avivi, A.; Neufeld, G.; Givol, D.; Yarden, Y.  
 Oncogene 6, 753-760, 1991  
 A/Title: PCR-based identification of new receptors: molecular cloning of a receptor for fibroblast growth factor  
 A/Reference number: S17295; PMID:91270892; PMID:1711190  
 A/Accession: S17295  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-820 <RAZ>  
 A/Cross-references: UNIPROT:P21803; EMBL:X55441; NID:950141; PIDN:CAA39083.1; PID:950142  
 C/Superfamily: Basic fibroblast growth factor receptor 1; Immunoglobulin homology; protein F/478-763/Domain: immunoglobulin homology <IMM>  
 F/478-763/Domain: protein kinase homology <KIN>

Query Match 9.9%; Score 111.5; DB 2; Length 820;  
 Best Local Similarity 25.9%; Pred. No. 0.11;  
 Matches 41; Conservative 23; Mismatches 55; Indels 39; Gaps 7;

Qy 83 EVSPFOGLRLOW-----NGSK-----DLQDVSTVL---NVLNDSC 116  
 Db 278 KYVSDAQPHQWIKHVKNGSKYGPDLPLKYLKKAAGVTTDKELVLRVTPEDAG 337  
 Qy 117 LYTCNVSRFEFEARPPVKTTRLPLRYTE-BAGEDFTSVSEIMMYILVFLTLMLE 175  
 Db 338 EYTCLAGNSIGISFHSAMW-TVLPAVREKEIRASPDYL---EIAIYCIQVGLIACMV 392  
 Qy 176 EMIYCYRKVSKAEAAQENASDYLAIPSENKENSAPVE 213  
 Db 393 TVIFCRMKITTKK-----PDFSQPAVHKLTAKIPL 423

## RESULT 14

TNMBX  
 fibroblast growth factor receptor bek precursor - mouse  
 N/Alternate names: bek transforming protein; fibroblast growth factor receptor 2; keratin N/Content: protein-tyrosine kinase (EC 2.7.1.112) bek  
 C/Species: Mus musculus (house mouse)  
 C/Date: 30-Jun-1991 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: A44142; A31378  
 R/Mansukhani, A.; Dell'Era, P.; Moscatelli, D.; Kornbluth, S.; Hanafusa, H.; Basilico, C Proc. Natl. Acad. Sci. U.S.A. 89, 3305-3309, 1992  
 A/Title: Characterization of the murine bek fibroblast growth factor (FGF) receptor: acti  
 A/Reference number: A44142; PMID:92228773; PMID:1373495  
 A/Accession: A44142

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar  
 A/Molecule type: mRNA  
 A/Residues: 1-821 <MAN>  
 A/Cross-references: UNIPROT:P21803; GB:M86441  
 R/Kornbluth, S.; Paulson, K.E.; Hanafusa, H. Mol. Cell. Biol. 8, 5541-5544, 1988  
 A/Title: Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA  
 A/Reference number: A31378; PMID:89219016; PMID:2468999  
 A/Accession: A31378  
 A/Molecule type: mRNA  
 A/Residues: 477-821 <KOR>  
 A/Cross-references: GB:M23362; NID:9533219; PIDN:AAA37285.1; PID:9533220  
 C/Genetics:

	C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
	C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor
F:/1-71/Domains:	signal sequence #status predicted <SIG>
F:/22-82/Product:	fibroblast growth factor receptor bek #status predicted <Mat>
F:/172-233/Domains:	immunoglobulin homology <IMW>
F:/378-398/Domains:	transmembrane #status predicted <IMW>
F:/479-764/Domains:	protein kinase homology <KIN>
F:/487-485/Region:	protein kinase ATP-binding motif
F:/62-107,179-231,278-342/Dissulfide bonds:	#status predicted
F:/83,123,147,241,265,297,318,331/Binding site:	carbohydrate
F:/517,534,626/Active site:	Lys, Glu, Asp #status predicted
F:/657/Binding site:	phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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Best Local Similarity	25.9%; Pred. No. 0.11;
Matches	41; Conservative 23; Mismatches 55; Indels 39; Gaps 7;
OY	83 EVESPPQGRLOW-----NGSK-----DLQVSYTVL---NNTLDSG 116
Dd	279 KVIYDQAQHIDMIKVENSGSKYGPDGLPYKLAKAGVNTTDKEIEVLRYRNVFEDAG 338
OY	117 LYTCNSREPEFEARHPVKTKTRLPLRVTE-EAGEPFTSVASEIMMYILLVPFTMLLI 175
Dd	339 EYTCLAGNSIGISPHSAWL-TVLPAPVAREKITSPDYLV----ELATCIGVFILACMV 393
OY	176 EMITCYRKRVSKAEBAQENASDIYLAIPEKNENSAPV 213
Dd	394 TVIFCRMKTKTK-----PDFSSQAPVHLTKRLIPL 424

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Db      5 YRMMSMLNIIILAY-IFLC-AICVOGSVKQEWAEIGKXVSLFCAS-----ENEA---VAN 54
Qy      63 FYRPEG-GKDFLIYEXNRNGHOEVESPFQGRLOQWNGSKDLQDV-----ITVANTLNDSG 116
Db      55 KLGNGQTINKNHTFRYKIRT-----EPLKSNDDGSENNDSDQFMKXKNVLTLLDVNINDSG 108
Qy      117 LRYC-----NYSREFEFANRPFVKTRRLIPLRYTEEAGSDFTSVSEIMMYILL 166
Db      109 NYTCTAQTGQNHSTEFQVKKPLP-SKVLQSTPDRIKRKIKOD-----VMLYCLI 156

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15  
 B36182  
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 N/Alternate names: protein-tyrosine-phosphatase DPTP  
 C/Species: Drosophila melanogaster  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: B36182  
 R/Streuli, M.; Krueger, N.X.; Teal, A.Y.M.; Saito, H.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989  
 A/Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila  
 A/Reference number: A36182; MUID:90046860; PMID:2554325  
 A/Accession: B36182  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-1462 <SNR>  
 A/Cross-references: UNIPROT:P16620; GB:M27699; NID:G158188; PIDN:AAA28842.1; PID:G158188  
 C/Genetics:  
 A/Gene: PTP69D  
 A/Cross-references: FlyBase:FBgn014007  
 C/Superfamily: protein-tyrosine-phosphatase, receptor type PTP69D, fibronectin type III phosphatase homology  
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane F.1-28/Domain: signal sequence #status predicted <SIG>  
 F.29-1462/Product: protein-tyrosine-phosphatase, receptor type PTP69D #status predicted  
 F.28-806/Domain: extracellular #status predicted <EXT>  
 F.38-114/Domain: immunoglobulin homology <IM>  
 F.147-216/Domain: immunoglobulin homology <IM2>  
 F.807-823/Domain: transmembrane #status predicted <TMN>  
 F.824-1462/Domain: intracellular #status predicted <INT>  
 F.917-1145/Domain: protein-tyrosine-phosphatase homology <PTP1>  
 F.1213-1439/Domain: protein-tyrosine-phosphatase homology <PTP2>  
 F.45-112,154-214/Disulfide bonds: #status predicted  
 F.1097/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F.1103/Binding site: substrate phosphate (Arg) #status predicted  
 F.1191/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F.1397/Binding site: substrate phosphate (Arg) #status predicted  
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 Best Local Similarity 26.7%; Pred. No. 0.25;  
 Matches 47; Conservative 31; Mismatches 61; Indels 37; Gaps 11;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:02:27 ; Search time 116 seconds  
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949.112 Million cell updates/sec

Title: US-09-977-579-2  
Perfect score: 1124  
Sequence: 1 MPFAFNRLPLASLVLYWVS.....SDYLAIPISENKENSAPVVE 215

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124	100.0	215	1	CIB3_HUMAN
2	1116	99.3	215	1	CIB3_MACFA
3	1105	98.3	215	1	CIB3_RAT
4	1097	97.6	215	1	CIB3_MOUSE
5	1097	97.6	268	2	Q692Q3
6	714	63.5	215	2	Q6DE47
7	477	42.4	218	1	CIB1_RABIT
8	472	42.0	218	1	CIB1_RAT
9	471	41.9	218	1	CIB1_HUMAN
10	468	41.6	218	1	CIB1_MOUSE
11	423	37.6	186	2	Q8WU42
12	262.5	23.4	273	2	Q9QXU3
13	258.5	23.0	268	2	Q6TN97
14	208	18.5	66	2	Q6TSE6
15	178.5	15.9	203	2	Q8TR56
16	172	15.6	248	1	MYPO_RAT
17	175	15.3	248	1	MYPO_MOUSE
18	163.5	14.5	209	2	Q6DDH9
19	163.5	14.5	248	1	MYPO_HUMAN
20	163.5	14.5	251	2	Q149J2
21	161.5	14.4	248	2	Q6WBS5
22	160.5	14.3	235	2	Q6UW72
23	159	14.1	219	1	MYPO_BOVIN
24	155	13.8	215	2	Q6NW73
25	150	13.3	202	2	Q914Q6
26	149	13.3	215	1	EVAI_MOUSE
27	147	13.1	215	1	EVAI_HUMAN
28	147	13.1	215	2	Q91W14
29	147	13.1	229	2	Q8AWV3
30	144.5	12.9	246	1	MYPO_HERF
31	140.5	12.5	249	1	MYPO_CHICK

32	131	11.7	243	2	Q9UEI4	Q9UEI4 homo sapien
33	131	11.7	269	2	Q95297	Q95297 homo sapien
34	130	11.6	270	2	Q6AYT8	Q6AYT8 rattus norv
35	127	11.3	183	2	Q9UEI6	Q9UEI6 homo sapien
36	127	11.3	209	2	Q9NYK4	Q9NYK4 homo sapien
37	125	11.1	199	2	Q8UG36	Q8UG36 brachydanio
38	125	11.1	202	2	Q8IX11	Q8IX11 homo sapien
39	125	11.1	209	2	Q6GQX5	Q6GQX5 mus musculu
40	122	10.9	233	2	Q8IX39	Q8IX39 homo sapien
41	121	10.8	287	2	Q9D7B8	Q9D7B8 mus musculu
42	118	10.5	215	1	CIB2_RAT	P54900 rattus norv
43	118	10.5	287	2	Q6SJ9P	Q6SJ9P mus musculu
44	117	10.4	186	2	Q62861	Q62861 rattus norv
45	116	10.3	222	2	Q8IX38	Q8IX38 homo sapien

#### ALIGNMENTS

RESULT 1  
CIB3\_HUMAN STANDARD; PRT; 215 AA.  
ID CIB3\_HUMAN  
AC Q9NY72; Q9ULR2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Sodium channel beta-3 subunit precursor.  
GN Name=SCN3B; Synonyms=KIAA1158;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20160948; PubMed=10688874; DOI=10.1073/pnas.030362197;  
RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,  
RA Plincock R.D., Hughes J., Richardson P.J., Mizuguchi K., Jackson A.P.;  
RT "beta3: an additional auxiliary subunit of the voltage-sensitive  
RT sodium channel that modulates channel gating with distinct kinetics.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Amygdala;  
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;  
RA Wiemann S., Weil B., Wellenreuther R., Gaessenhuber J., Glaesl S.,  
RA Amsorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,  
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,  
RA Meuser H.-W., Ottenmaier B., Obermaier B., Tampe J., Heubner D.,  
RA Wambutt R., Korn B., Klein M., Pouskka A.;  
RT "Towards a catalog of human genes and proteins: sequencing and  
RT analysis of 500 novel complete protein coding human cDNAs.";  
RN Genome Res. 11:422-435(2001).  
RP [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20039618; PubMed=10574461;  
RA Hirosewa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,  
RA Ohara O.;  
RT "Characterization of cDNA clones selected by the Genemark analysis  
RT from size-fractionated cDNA libraries from human brain.";  
RN DNA Res. 6:329-336(1999).  
RL -1- FUNCTION: Modulates channel kinetics. Causes unique  
CC persistent sodium currents. Inactivates the sodium channel opening  
CC slower than the beta-1 subunit. Its association with neurofascin  
CC may target the sodium channels to the nodes of Ranvier of  
CC developing axons and retain these channels at the nodes in mature  
CC myelinated axons (By similarity).  
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
CC conducting pore forming alpha-subunit regulated by one or more  
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are  
CC noncovalently associated with alpha, while beta-2 is covalently  
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate

with neurofascin (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

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EMBL; AJ243396; CAB76825.1; -

EMBL; AB136589; CAB6524.1; -

EMBL; AB032984; BAA86472.1; ALT\_INT.

HSSP; P06907; INEU.

GeneW; HGNC:20665; SCN3B.

H-invdB; HIX0010216; -

MIM; 608214; -

GO; GO:0016021; C:integral to membrane; NAS.

GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.

GO; GO:0006814; P:sodium ion transport; NAS.

InterPro; IPR007110; Ig-like.

Pfam; PF00047; Ig\_1.

PROSITE; PS50835; IG\_LIKE; 1.

Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane; Voltage-gated channel.

SIGNAL 1 22

CHAIN 23 215 Sodium channel beta-3 subunit.

DOMAIN 23 159 Extracellular (Potential).

TRANSMEM 160 180 Cytoplasmic (Potential).

DOMAIN 181 215 Ig-like C2-type.

DISULFID 26 48 Potential.

DISULFID 45 120 Potential.

CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).

CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).

CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).

CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).

SEQUENCE 215 AA; 24702 MW; 70F6C604B9E26662 CRC64;

Query Match 100.0%; Score 1124; DB 1; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.le-93;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFRLPLSLVLIYVSVCFVCEVPSSTEAQVQPMKLRICSCMKREVEATTIV 60

DB 1 MPAFRLPLSLVLIYVSVCFVCEVPSSTEAQVQPMKLRICSCMKREVEATTIV 60

QY 61 EWFYRPEGGKDFLIYERNHGOEVESPFQGRLOWNGSKDLDVSTIVLVNTLNSGLYTC 120

DB 61 EWFYRPEGGKDFLIYERNHGOEVESPFQGRLOWNGSKDLDVSTIVLVNTLNSGLYTC 120

QY 121 NVSRFEFPAHPPFKYTRRLPLRTEAGDEFTSVSEIMMYILVFLTLLLEMYIC 180

DB 121 NVSRFEFPAHPPFKYTRRLPLRTEAGDEFTSVSEIMMYILVFLTLLLEMYIC 180

QY 181 YRKVSKAEAAQENASDYLAIPSENKENSAYPVEE 215

DB 181 YRKVSKAEAAQENASDYLAIPSENKENSAYPVEE 215

RESULT 2

CIB3\_MACFA STANDARD; PRT; 215 AA.

AC Q8HXY7;

DT 29-MAR-2004 (rel. 43, Created)

DT 29-MAR-2004 (rel. 43, Last sequence update)

DT 25-OCT-2004 (rel. 45, Last annotation update)

DE Sodium channel beta-3 subunit precursor (Qmoa-13657).

GN Name=SCN3B;

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopitheciinae; Macaca.

NCBI\_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISUE-Medulla oblongata;

RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Modulates channel gating kinetics. Causes unique persistent sodium currents. Inactivates the sodium channel opening slower than the beta-1 subunit. Its association with neurofascin may target the sodium channels to the nodes of Ranvier of developing axons and retain these channels at the nodes in mature myelinated axons (By similarity).

-1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion conducting pore forming alpha-subunit regulated by one or more beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are noncovalently associated with alpha, while beta-2 is covalently linked by disulfide bonds. Beta-1 or beta-3 subunits associate with neurofascin (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

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-----

EMBL; AB097521; BAC41746.1; -

HSSP; P06907; INEU.

InterPro; IPR007110; Ig-like.

Pfam; PF00047; Ig\_1.

PROSITE; PS50835; IG\_LIKE; 1.

Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane; Voltage-gated channel.

SIGNAL 1 22

CHAIN 23 215 Sodium channel beta-3 subunit.

DOMAIN 23 159 Extracellular (Potential).

TRANSMEM 160 180 Potential.

DOMAIN 181 215 Cytoplasmic (Potential).

DOMAIN 24 138 Ig-like C2-type.

DISULFID 26 48 Potential.

DISULFID 45 120 Potential.

CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).

CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).

CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).

CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).

SEQUENCE 215 AA; 24702 MW; 25319D5ED218AACF CRC64;

Query Match 99.3%; Score 1116; DB 1; Length 215;

Best Local Similarity 99.1%; Pred. No. 6e-93;

Matches 213; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPAFRLPLSLVLIYVSVCFVCEVPSSTEAQVQPMKLRICSCMKREVEATTIV 60

DB 1 MPAFRLPLSLVLIYVSVCFVCEVPSSTEAQVQPMKLRICSCMKREVEATTIV 60

QY 61 EWFYRPEGGKDFLIYERNHGOEVESPFQGRLOWNGSKDLDVSTIVLVNTLNSGLYTC 120

DB 61 EWFYRPEGGKDFLIYERNHGOEVESPFQGRLOWNGSKDLDVSTIVLVNTLNSGLYTC 120

QY 121 NVSRFEFPAHPPFKYTRRLPLRTEAGDEFTSVSEIMMYILVFLTLLLEMYIC 180

DB 121 NVSRFEFPAHPPFKYTRRLPLRTEAGDEFTSVSEIMMYILVFLTLLLEMYIC 180

QY 181 YRKVSKAEAAQENASDYLAIPSENKENSAYPVEE 215

DB 181 YRKVSKAEAAQENASDYLAIPSENKENSAYPVEE 215



RESULT 3  
CIB3\_RAT STANDARD; PRT; 215 AA.  
AC 09JRK0;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Sodium channel beta-3 subunit precursor.  
GN Name=Scn3b;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND PROBABLE DISULFIDE BONDS.  
RC TISSUE=Brain;  
RX MEDLINE=20160948; PubMed=10688874; DOI=10.1073/pnas.030362197;  
RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,  
RA Pincock R.D., Hughes J., Richardson P.J., Mizuguchi K., Jackson A.P.;  
RT "Beta3: an additional auxiliary subunit of the voltage-sensitive  
RT sodium channel that modulates channel gating with distinct kinetics.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).  
RN [2]  
RP SEQUENCE FROM N.A., CHARACTERIZATION, TISSUE SPECIFICITY, AND SUBUNIT.  
RC STRAIN=Sprague-Dawley; TISSUE=Dorsal root ganglion;  
RX MEDLINE=21919106; PubMed=11922146; DOI=10.1006/mcne.2001.1039;  
RA Xu Y., Curtis R., Lawson D., Glibridse K., Ge P., Distefano P.S.,  
RA Silow-Santiago I., Caterall W.A., Schener T.;  
RT "Differential modulation of sodium channel gating and persistent  
RT sodium currents by the beta1, beta2, and beta3 subunits.";  
RL Mol. Cell. Neurosci. 18:570-580(2001).  
RN [3]  
RP INTERACTION WITH NEUROFASCIN  
RX MEDLINE=21363577; PubMed=11470829; DOI=10.1083/jcb.200102086;  
RA Ratcliffe C.F., Westbroek R.E., Curtis R., Caterall W.A.;  
RT "Sodium channel beta1 and beta3 subunits associate with neurofascin  
RT through their extracellular immunoglobulin-like domain.";  
RL J. Cell Biol. 154:427-434(2001).  
RN [4]  
RP FUNCTION: Modulates channel gating kinetics. Causes unique  
CC persistent sodium currents. Inactivates the sodium channel opening  
CC slower than the beta-1 subunit. Its association with neurofascin  
CC may target the sodium channels to the nodes of Ranvier of  
CC developing axons and retain these channels at the nodes in mature  
CC myelinated axons.  
CC  
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
CC conducting pore forming alpha-subunit regulated by one or more  
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are  
CC noncovalently associated with alpha, while beta-2 is covalently  
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate  
CC with neurofascin.  
CC  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC  
CC -1- TISSUE SPECIFICITY: Expressed broadly in neurons in the central  
CC and peripheral nervous systems, but not in glia and most  
CC nonneuronal cells. Weak detection in lung and adrenal gland.  
CC  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AJ243395; CAB76838.1; -  
CC EMBL: AF378093; AAK5415.1; -  
CC HSSP: P06907; INEU  
CC InterPro: IPR007110; Ig-like.  
CC Pfam: PF00047; Ig\_1.  
CC PROSITE: PS50835; IG\_LIKE\_1.  
KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;  
KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.  
FT SIGNAL 1 24 Potential.

FT CHAIN 25 215 Sodium channel beta-3 subunit.  
FT DOMAIN 25 159 Extracellular (Potential).  
FT TRANSMEM 160 180 Potential.  
FT CYTOPLASM 181 215 Cytoplasmic (Potential).  
FT DOMAIN 25 138 Ig-like C2-type.  
FT DISULFID 26 48 Potential.  
FT CARBOHYD 45 120 Potential.  
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 215 AA; 24799 MW; 05684885E5AEF4F CRC64;  
  
Query Match 98.3%; Score 1105; DB 1; Length 215;  
Best Local Similarity 98.1%; Pred. No. 6e-92;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 MPAENRLLPLASLVLYWVSCPEVCVPSSETEAVQGNPMKRCISCMKREEVATTV 60  
DB 1 MPAENRLLPLASLVLYWVSCPEVCVPSSETEAVQGNPMKRCISCMKREEVATTV 60  
  
QY 61 EWFYRPGGKDFLIYERNGHGVESPFQGRLOMNSKDIQDVSYTANTLNDGLYTC 120  
DB 61 EWFYRPGGKDFLIYERNGHGVESPFQGRLOMNSKDIQDVSYTANTLNDGLYTC 120  
  
QY 121 NVSRPEPEAHKPFVKTTRLPLRVTEAGEDFTSVSEIMTYLTLVFLTLMLLIEMTYC 180  
DB 121 NVSRPEPEAHKPFVKTTRLPLRVTEAGEDFTSVSEIMTYLTLVFLTLMLLIEMTYC 180  
  
QY 181 YRKVSKAEBAQENASDYLAIPSENKNSAVPEE 215  
DB 181 YRKVSKAEBAQENASDYLAIPSENKNSAVPEE 215  
  
RESULT 4  
CIB3\_MOUSE STANDARD; PRT; 215 AA.  
AC 08BHK2; 091299;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Sodium channel beta-3 subunit precursor.  
GN Name=Scn3b;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head, and Spinal cord;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,  
RA Niki K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gofjorci T.,  
RA Baldirelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schirral L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chottha C., Corbani L.E., Cousins S.,  
RA Dalia E., Dragani T.A., Fletcher C.F., Fortes A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa Y., Kozuka I., Kiyosawa H.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurouchkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilmig L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zevolan M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aikawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RT Nature 420:563-573 (2002).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Brain, and Olfactory epithelium;  
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McQuellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -1- FUNCTION: Modulates channel gating kinetics. Causes unique  
CC persistent sodium currents. Inactivates the sodium channel opening  
CC slowlier than the beta-1 subunit. Its association with neurofascin  
CC may target the sodium channels to the nodes of Ranvier of  
CC developing axons and retain these channels at the nodes in mature  
CC myelinated axons (By similarity).  
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
CC conducting pore forming alpha-subunit regulated by one or more  
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are  
CC noncovalently associated with alpha, while beta-2 is covalently  
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate  
CC with neurofascin (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -----  
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CC -----  
CC EMBL, AY049036; AAL07512.1; -;  
CC EMBL, AK049747; BAC33901.1; -;  
CC EMBL, AK076466; BAC36356.1; -;  
CC EMBL, BC053919; AAH53919.1; -;  
CC EMBL, BC058636; AAH58636.1; -;  
CC HSSP, P06907; INED.  
CC MGD, MGI:1918882; Scn3b.  
CC InterPro, IPR007110; Ig\_1-like.  
CC Pfam, PF00047; Ig\_1.  
CC PROSITE, PSS0835; IG\_LIKE; 1.  
CC Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;  
CC Signal; Sodium channel; Transmembrane; Voltage-gated channel.  
CC SIGNAL 1 24  
CC CHAIN 25 215 Sodium channel beta-3 subunit.

FT DOMAIN 25 159 Extracellular (Potential).  
FT TRANSMEM 160 180 Potential.  
FT DOMAIN 181 215 Cytoplasmic (Potential).  
FT DOMAIN 25 138 Ig-like C2-type.  
FT DISULFID 26 48 Potential.  
FT DISULFID 45 120 Potential.  
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 215 AA; 24789 MW; 0E07B47041784423 CRC64;

Query Match 97.6%; Score 1097; DB 1; Length 215;  
Best Local Similarity 97.7%; Pred. No. 3, 2e-91;  
Matches 210; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVLIYWSVCFPCVPEVSTEAQNGNPKLRICSKKREVEATTV 60  
DB 1 MPAFRLPLASLVLIYWSVCFPCVPEVSTEAQNGNPKLRICSKKREVEATTV 60  
QY 61 EHFYRPEGKDFLIYERNRNGHOEVSPFOGRLOMNGSKDLODVSTLVNTLNDGLYTC 120  
DB 61 EHFYRPEGKDFLIYERNRNGHOEVSPFOGRLOMNGSKDLODVSTLVNTLNDGLYTC 120  
QY 121 NVSRFEFEAPRRPVKTRRLPLRVTEAGDEDFTSVSEIMVYILVFLTLMLIEMTYC 180  
DB 121 NVSRFEFEAPRRPVKTRRLPLRVTEAGDEDFTSVSEIMVYILVFLTLMLIEMTYC 180  
QY 181 YRKVSKEBPAQENSDVLAISPKENKSAVVEE 215  
DB 181 YRKVSKEBPAQENSDVLAISPKENKSAVVEE 215

RESULT 5  
Q69ZQ3 PRELIMINARY; PRT; 268 AA.

AC Q69ZQ3;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, last annotation update)  
DE MKIAA1158 protein (Fragment).  
GN Name=MKIAA1158;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
RA Suga Y., Seino S., Nishimura M., Katsuo T., Hoshino K., Kitamura H.,  
RA Nagase T., Ohara O., Koga H.;  
RT "Prediction of the Coding Sequences of Mouse Homologues of KIA Gene:  
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIA-Homologous  
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones  
RT Randomly Sampled from Size-Fractionated Libraries";  
RL DNA Res. 11:205-218 (2004).  
DR EMBL, AK173115; BAD3393.1; -;  
DR InterPro, IPR003599; Ig\_1-like.  
DR InterPro, IPR007110; Ig\_1-like.  
DR InterPro, IPR003596; Ig\_v.  
DR Pfam, PF00047; Ig\_1.  
DR SMART, SM00409; IG\_1.  
DR SMART, SM00406; IGV\_1.  
DR PROSITE, PSS0835; IG\_LIKE; 1.

FT NON\_TER 1  
SQ SEQUENCE 268 AA; 30330 MW; 7A2655D5DD2409F CRC64;

Query Match 97.6%; Score 1097; DB 2; Length 268;  
Best Local Similarity 97.7%; Pred. No. 4, 1e-91;  
Matches 210; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVLIYWSVCFPCVPEVSTEAQNGNPKLRICSKKREVEATTV 60  
|||||

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Db      54 MPAFNRLPLASLVLIYMWVCPVCVEPSETEAVOGNSMKLRICISCMKREVEATTVV 113
QY      61 EMFYREPGKDFLIYEXRNHGVESPFQRLQWNSKDIQDVSIITVANTLNDGSLYTC 120
Db      114 EMFYREPGKDFLIYEXRNHGVESPFQRLQWNSKDIQDVSIITVANTLNDGSLYTC 173
QY      121 NVSRFEFPAHRRPFVKTRILPLRVTEAGEDFTSVSEIMMYILLVFLTMLLIEMIYC 180
Db      174 NVSRFEFPAHRRPFVKTRILPLRVTEAGEDFTSVSEIMMYILLVFLTMLLIEMIYC 233
QY      181 YRKVSKAEAAQENASDYLAIPSENKENSAPVEE 215
Db      234 YRKVSKAEAAQENASDYLAIPSENKENSAPVEE 268

RESULT 6
Q6DE47  PRELIMINARY; PRT; 215 AA.
AC      25-OCT-2004 (T-EMBLrel. 28, Created)
DT      25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE      25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
GN      Name=scn3b-prov;
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC      Xenopodinae; Xenopus.
NCBI    NCBI_TaxID=8355;
RN      [1]
RP      TISSUE=Embryo;
RC      MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dady.10174;
RA      Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RT      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT      initiative.";
RT      Dev. Dyn. 225:384-391(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RC      PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Spelman C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Datchenko L., Matovina K., Farmer A.A., Rubin J.L., Scheetz T.E.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Maita M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RT      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RC      Klein S., Gerhard D.S.;
RT      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL: BC077295; AAH77295.1; -.
DR      InterPro: IPR003599; IG.
DR      InterPro: IPR007110; IG-like.
DR      InterPro: IPR003596; IG_v.
DR      SMART: SM00409; IG_1.
DR      SMART: SM00406; IG_v_1.

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DR      PROSITE; PS50835; IG LIKE; 1.
SQ      SEQUENCE 215 AA; 24472 MW; 2AAB890E46DE0289 CRC64;
Query Match 63.5%; Score 714; DB 2; Length 215;
Best Local Similarity 62.8%; Pred. No. 1.ee-56;
Matches 135; Conservative 32; Mismatches 48; Indels 0; Gaps 0;

QY      1 MPAFNRLPLASLVLIYMWVCPVCVEPSETEAVOGNSMKLRICISCMKREVEATTVV 60
Db      1 MAAMENIFWTDVSLFLMVFCSFVCVEQSGTEAVGEMNTLLCISCMKREVEAATTNV 60
QY      61 EMFYREPGKDFLIYEXRNHGVESPFQRLQWNSKDIQDVSIITVANTLNDGSLYTC 120
Db      61 RMFYQPDGGEILYEDGKPLDKSPLOQRLQWNSKDIQDVSIITVANTLNDGSLYTC 120
QY      121 NVSRFEFPAHRRPFVKTRILPLRVTEAGEDFTSVSEIMMYILLVFLTMLLIEMIYC 180
Db      121 HNVRTLHFDHHRSTQSKSITLKVMEAGEDFTSVSKIMMYILLVFLTMLLVEVAYC 180
QY      181 YRKVSKAEAAQENASDYLAIPSENKENSAPVEE 215
Db      181 YRKISKAEAEVQESVTDYLAIPSENKENSAPVEE 215

RESULT 7
CIBI_RABIT STANDARD; PRT; 218 AA.
AC      P53788;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DE      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Sodium channel beta-1 subunit precursor.
GN      Name=SCN1B;
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI    NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=New Zealand white; TISSUE=Sciatic nerve;
RA      MEDLINE=96235151; PubMed=8666261; DOI=10.1016/0378-1119(95)00871-3;
RA      Belcher S.M., Howe J.R.;
RT      "Cloning of the cDNA encoding the sodium channel beta 1 subunit from
RT      rabbit.";
RT      Gene 170:285-286(1996).
RN      [2]
RP      FUNCTION: Crucial in the assembly, expression, and functional
RP      modulation of the heterotrimeric complex of the sodium channel.
RP      The beta-1 subunit can modulate multiple alpha subunit isoforms
RP      from brain, skeletal muscle, and heart. Its association with
RP      neurofascin may target the sodium channels to the nodes of Ranvier
RP      of developing axons and retain these channels at the nodes in
RP      mature myelinated axons (By similarity).
CC      -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
CC      conducting pore forming alpha-subunit regulated by one or more
CC      beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
CC      associated with alpha, while beta-2 is covalently linked by
CC      disulfide bonds. Beta-1 or beta-3 subunits associate with
CC      neurofascin (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: J05382; AAB17572.1; -.
DR      PIR: JC4788; JC4788.
DR      InterPro: IPR007110; IG-like.
DR      Pfam: PF00047; IG_1.

```

DR PROSITE; P550835; IG LIKE; FALSE NEG.  
 KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;  
 KM Signal; Sodium channel; Transmembrane; Voltage-gated channel.  
 FT SIGNAL 1 18 By similarity. beta-1 subunit.  
 FT CHAIN 19 218 Sodium channel beta-1 subunit.  
 FT DOMAIN 19 160 Extracellular (Potential).  
 FT TRANSMEM 161 182 Potential.  
 FT DOMAIN 183 218 Cytoplasmic (Potential).  
 FT DOMAIN 22 150 Ig-like C2-type.  
 FT DISULFID 21 43 Potential.  
 FT DISULFID 40 121 Potential.  
 FT CARBOHYD 93 93 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 110 110 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 114 114 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 135 135 N-linked (GlcNAc . . .) (Potential).  
 SQ SEQUENCE 218 AA, 24706 MW, 39BD174E1FAE7FD2 CRC64;  
 Query Match 42.4%; Score 477; DB 1; Length 218;  
 Best Local Similarity 49.5%; Pred. No. 4,6e-35;  
 Matches 106; Conservative 32; Mismatches 68; Indels 8; Gaps 5;  
 QY 10 LASLVLIYVWSYCFVCEVPESETAVOQNPMLKACISCKRKEVEATTVEMFYRPEGG 69  
 DB 5 LAFVVGALVSSAWGCVDETEAVYGMTEFKLICISCKRSEETAEFTETWTRQKGT 64  
 QY 70 KDFL-IYEVYRNGHOVESP--FOGRLQWNGS---KDLQDVSTVLTNVLNDSGLYTCNVS 123  
 DB 65 BEFVKILRYENEVNQLQLEDEREPRGVWNGSGTDLQDLSTFINVTYNHSGDYQCHYV 124  
 QY 124 REFEFAHPPVYKTRLLPLRVTBEGEDFTSVSEIMWYLLVPLTLLILEMYYCYRK 183  
 DB 125 RLSEFNEHNTSVYVKIHLFVDRKANRDMASIVSEIMWYLLVPLTLLVLEMYCYRK 184  
 QY 184 VSKA-EAAQENASDYLAIPSENKEN-SAVPYEE 215  
 DB 185 IAAATEAAQENASDYLAIPSENKENCTGVQVAE 218  
 RESULT 8  
 CIB1\_RAT STANDARD; PRT; 218 AA.  
 AC Q00954;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Sodium channel beta-1 subunit precursor.  
 DE Name=Scn1b;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Brain;  
 RA MEDLINE=92271207; PubMed=1375395;  
 RA Isom L.L., De Jongh K.S., Patton D.E., Reber B.F.X., Offord J.,  
 RA Charbonneau H., Welsh K., Goldin A.L., Catterall W.A.;  
 RA "Primary structure and functional expression of the beta 1 subunit of  
 RT the rat brain sodium channel.";  
 RL Science 256:839-842(1992).  
 RN [2]  
 RP INTERACTION WITH NEUROFASCIN.  
 RX MEDLINE=21363577; PubMed=11470829; DOI=10.1083/jcb.200102086;  
 RA Ratcliffe C.F., Westenbroek R.E., Curtis R., Catterall W.A.;  
 RA "Sodium channel beta1 and beta3 subunits associate with neurofascin  
 RT through their extracellular immunoglobulin-like domain.";  
 RL J. Cell Biol. 154:427-434(2001).  
 CC -!- FUNCTION: Crucial in the assembly, expression, and functional  
 CC modulation of the heterotrimeric complex of the sodium isoforms  
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms  
 CC from brain, skeletal muscle, and heart. Its association with  
 CC neurofascin may target the sodium channels to the nodes of Ranvier  
 CC of developing axons and retain these channels at the nodes in

CC mature myelinated axons.  
 CC -!- SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
 CC conducting pore forming alpha-subunit regulated by one or more  
 CC beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently  
 CC associated with alpha, while beta-2 is covalently linked by  
 CC disulfide bonds. Beta-1 or beta-3 subunits associate with  
 CC neurofascin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in brain, heart, skeletal muscle and  
 CC spinal cord.  
 CC -!- DEVELOPMENTAL STAGE: In developing nodes of Ranvier, it is  
 CC localized in the sciatic nerve at postnatal days 3 and 10, during  
 CC the process of myelination and maturation of the nodes.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
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 CC  
 CC EMBL; M91808; AAA88513.1; -;  
 DR PIR; A42737; A42737.  
 DR RGD; 3631; Scn1b.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig\_1.  
 DR PROSITE; P550835; IG LIKE; FALSE NEG.  
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;  
 KW Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane;  
 KW Voltage-gated channel.  
 FT SIGNAL 1 18  
 FT CHAIN 19 218 Sodium channel beta-1 subunit.  
 FT DOMAIN 19 160 Extracellular (Potential).  
 FT TRANSMEM 161 182 Potential.  
 FT DOMAIN 183 218 Cytoplasmic (Potential).  
 FT DOMAIN 22 150 Ig-like C2-type.  
 FT DISULFID 21 43 Potential.  
 FT DISULFID 40 121 Potential.  
 FT CARBOHYD 93 93 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 110 110 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 114 114 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 135 135 N-linked (GlcNAc . . .) (Potential).  
 SQ SEQUENCE 218 AA, 24692 MW, 0BA84FC44FP2306B CRC64;  
 Query Match 42.0%; Score 472; DB 1; Length 218;  
 Best Local Similarity 49.1%; Pred. No. 1.3e-34;  
 Matches 105; Conservative 33; Mismatches 68; Indels 8; Gaps 5;  
 QY 10 LASLVLIYVWSYCFVCEVPESETAVOQNPMLKACISCKRKEVEATTVEMFYRPEGG 69  
 DB 5 LAFVVGALVSSAWGCVDETEAVYGMTEFKLICISCKRSEETAEFTETWTRQKGT 64  
 QY 70 KDFL-IYEVYRNGHOVESP--FOGRLQWNGS---KDLQDVSTVLTNVLNDSGLYTCNVS 123  
 DB 65 BEFVKILRYENEVNQLQLEDEREPRGVWNGSGTDLQDLSTFINVTYNHSGDYQCHYV 124  
 QY 124 REFEFAHPPVYKTRLLPLRVTBEGEDFTSVSEIMWYLLVPLTLLILEMYYCYRK 183  
 DB 125 RLSEFNEHNTSVYVKIHLFVDRKANRDMASIVSEIMWYLLVPLTLLVLEMYCYRK 184  
 QY 184 VSKA-EAAQENASDYLAIPSENKEN-SAVPYEE 215  
 DB 185 IAAATEAAQENASDYLAIPSENKENCTGVQVAE 218  
 RESULT 9  
 CIB1\_HUMAN STANDARD; PRT; 218 AA.  
 AC Q07699;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Sodium channel beta-1 subunit precursor.  
 GN Name=SCN1B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93357746; PubMed=8394762;  
 RA McClatchey A.I., Cannon S.C., Staugenhardt S.A., Guseella J.F.;  
 RT "The cloning and expression of a sodium channel beta 1-subunit cDNA  
 from human brain.";  
 RL Hum. Mol. Genet. 2:745-749(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart, and Skeletal muscle;  
 RX MEDLINE=94171787; PubMed=8125980;  
 RA Makita N., Bennett P.B. Jr., George A.L. Jr.;  
 RT "Voltage-gated Na+ channel beta 1 subunit mRNA expressed in adult  
 human skeletal muscle, heart, and brain is encoded by a single gene.";  
 RL J. Biol. Chem. 269:7571-7578(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=95154833; PubMed=7851891;  
 RA Makita N., Sloan-Brown K., Weghuis D.O., Rogers H.-H.,  
 George A.L. Jr.;  
 RT "Genomic organization and chromosome assignment of the human voltage-  
 gated Na+ channel beta 1 subunit gene (SCN1B).";  
 RL Genomics 23:628-634(1994).  
 RN [4]  
 RP VARIANT GERS+ TRP-121.  
 RX MEDLINE=98361163; PubMed=9697698; DOI=10.1038/1252;  
 RA Wallace R.H., Wang D.W., Singh R., Schaffer I.E., George A.L. Jr.,  
 Phillips H.A., Saar K., Reis A., Johnson E.W., Sutherland G.R.,  
 Berkovic S.F., Mulley J.C.;  
 RT "Refrile seizures and generalized epilepsy associated with a mutation  
 in the Na(+)-channel beta-1 subunit gene SCN1B.";  
 RL Nat. Genet. 19:366-370(1998).  
 CC -1- FUNCTION: Crucial in the assembly, expression, and functional  
 modulation of the heterotrimeric complex of the sodium channel.  
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms  
 from brain, skeletal muscle, and heart. Its association with  
 neurofascin may target the sodium channels to the nodes of Ranvier  
 of developing axons and retain these channels at the nodes in  
 mature myelinated axons.  
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
 conducting pore forming alpha-subunit regulated by one or more  
 beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently  
 associated with alpha, while beta-2 is covalently linked by  
 disulfide bonds. Beta-1 or beta-3 subunits associate with  
 neurofascin.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, heart  
 and brain.  
 CC -1- DISEASE: Defects in SCN1B are a cause of generalized epilepsy with  
 febrile seizures plus (GEFS+) [MIM:604233]. GEFS+ is a disease  
 characterized by a highly variable phenotype combining febrile  
 seizures, generalized seizures often precipitated by fever at age  
 6 years or more, and partial seizures, with a variable degree of  
 severity.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
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DR EMBL: L10338; AAA60391.1; -;  
 DR EMBL: L16242; AAA61277.1; -;  
 DR EMBL: U12193; AAB97608.1; -;  
 DR EMBL: U12189; AAB97608.1; JOINED.  
 DR EMBL: U12190; AAB97608.1; JOINED.  
 DR EMBL: U12191; AAB97608.1; JOINED.  
 DR EMBL: U12192; AAB97608.1; JOINED.  
 DR PIR: A55734; A55734.  
 DR Genew; HGNC:10586; SCN1B.  
 DR MIM: 600235; -;  
 DR MIM: 604233; -;  
 DR GO: GO:0005248; F: voltage-gated sodium channel activity; TAS.  
 DR GO: GO:0006814; P: sodium ion transport; TAS.  
 DR GO: GO:0007268; P: synaptic transmission; TAS.  
 DR InterPro: IPR007110; I9-like.  
 DR Pfam: PF00047; I9; 1.  
 DR PROSITE: PS50835; IG\_LIKE, FALSE\_NEG.  
 KW Disease mutation; Epilepsy; Glycoprotein; Immunoglobulin domain;  
 KW Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane;  
 KW Voltage-gated channel.  
 FT SIGNAL 1 18  
 FT CHAIN 19 218  
 FT DOMAIN 19 160  
 FT TRANSMEM 161 182  
 FT DOMAIN 183 218  
 FT DOMAIN 22 150  
 FT DISULFID 21 43  
 FT CARBOHYD 93 93  
 FT CARBOHYD 110 110  
 FT CARBOHYD 114 114  
 FT CARBOHYD 135 135  
 FT VARIANT 121 121  
 FT C->W (in GEFS+).  
 FT FTID=VAR\_010165.  
 SQ SEQUENCE 218 AA; 24707 MW; 09B812FA3F9E9018 CRC64;  
 Query Match 41.9%; Score 471; DB 1; Length 218;  
 Best Local Similarity 49.5%; Pred. No. 1.6e-34;  
 Matches 106; Conservative 31; Mismatches 69; Indels 8; Gaps 5;  
 QY 10 LASVLILYVWSVCFPVCEVPESETEAVQGNPMKLRCSCKMKREVEATVWEMFPEEGC 69  
 DB 5 LALVVGALVSSACGCGVEVDSETEAVYGMTPILICISCRSRSTNAETFTWTFRQKT 64  
 QY 70 KDFL-IYEYNGHOEVSF--FGRLQWNGS---KDIQVSYLVANTLNDGLTYCNVS 123  
 DB 65 EEEVKILRYENEVLQLEDEDERFEGRVVWNGSRGKQIDLSIFITVNTYHSGDYECHVY 124  
 QY 124 REEFPEAHRFVFTTRILPLRVTEBEGEDFTSVSEIMTYLILVFLMLIEMTYCYRK 183  
 DB 125 RLFPFENEHTNSVKKIHLEVDKARDMASIVSEIMTYLVLTIVLVAEMTYCYRK 184  
 QY 184 VSKA-EEAAQENASDYLAIPESENEN-SAVPEE 215  
 DB 185 IAAATETPAQENASEYLAITSEKENCTGVQVAE 218  
 RESULT 10  
 CIB1 MOUSE STANDARD; PRT; 218 AA.  
 ID CIB1 MOUSE  
 AC P97953;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Sodium channel beta-1 subunit precursor.  
 GN Name=Scn1b;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=97156884; PubMed=9013777; DOI=10.1016/S0169-328X(96)00123-4;  
 RA Grosen C.L.S., Cannon S.C., Corey D.P., Gussella J.F.;  
 RT "Sequence of the voltage-gated sodium channel beta1-subunit in wild-  
 RT type and in quivering mice."; Brain Res. Mol. Brain Res. 42:222-226(1996).  
 RL Brain Res. Mol. Brain Res. 42:222-226(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96837156; PubMed=9721701;  
 RA Kuperawid S., Yang T., Roden D.M.;  
 RT "Mutation of cardiac Na+ current phenotype by beta1-subunit  
 RT expression."; Circ. Res. 83:441-447(1998).  
 RL [3]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Caeavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley D.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [1]  
 CC -1- FUNCTION: Crucial in the assembly, expression, and functional  
 CC modulation of the heterotrimeric complex of the sodium channel.  
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms  
 CC from brain, skeletal muscle, and heart. Its association with  
 CC neurofascin may target the sodium channels to the nodes of Ranvier  
 CC of developing axons and retain these channels at the nodes in  
 CC mature myelinated axons (By similarity).  
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion  
 CC conducting pore forming alpha-subunit regulated by one or more  
 CC beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently  
 CC associated with alpha, while beta-2 is covalently linked by  
 CC disulfide bonds. Beta-1 or beta-3 subunits associate with  
 CC neurofascin (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC  
 CC -----  
 CC EMBL: U46681; AAC53006.1; -;  
 CC EMBL: U85786; AAB49368.1; -;  
 CC EMBL: BC009652; AAB09652.1; -;  
 CC EMBL: BC039140; AAB39140.1; -;  
 CC MGI: MGI:98247; Scn1b.  
 CC InterPro: IPR007110; Ig-like.  
 CC Pfam: PF00047; Ig\_1.  
 CC PROSITE: PS00835; IG\_LIKE; FALSE NEG.  
 KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;  
 KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.  
 FT SIGNAL 1 18 By similarity.  
 FT CHAIN 19 218 Sodium channel beta-1 subunit.  
 FT DOMAIN 19 160 Extracellular (Potential).

FT TRANSMEM 161 182 Potential.  
 FT DOMAIN 183 218 Cytoplasmic (Potential).  
 FT SIGNAL 22 150 Ig-like C2-type.  
 FT DISULFID 21 43 Potential.  
 FT DISULFID 40 121 Potential.  
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 218 AA; 24650 MW; 5198f383b0a8ca5 CRC64;  
 Query Match 41.6%; Score 468; DB 1; Length 218;  
 Best Local Similarity 48.6%; Pred. No. 3e-34;  
 Matches 104; Conservative 34; Mismatches 68; Indels 8; Gaps 5;  
 QY 10 LASLVLTIVWSYCFVYCVHVESETAVVQGNPKKACISCKMREBEATTVWEMFRREG 69  
 DB 5 LALVGAALVSSAWGCVVEVDSTAVYGMTFKILICISCKRSEFTAEFTETMRKGT 64  
 QY 70 KDPL-IYEVNNGHOVESP--FQGRLOWNGS---KDLQDVSTIVNTLNDGLTYCNVS 123  
 DB 65 BEFVILTYNENHVDLEDDEFRGVNNGSRGTDLDDLSFITNVYTNHSGDYECHY 124  
 QY 124 REFEEHARRPFVKTTRLPLRVTEBAGDFTSVSEIMVYLLVFLTLLIEMTYCYRK 183  
 DB 125 RLFPDNEYHNTSVVKIHLBVDKRNDRMVASIVSEIMVYLLVLTLLVLAEMVYCYRK 184  
 QY 184 VSKA-EAAQENASDYLAIPSENKEN-SAVPPEE 215  
 DB 185 IAAATEAAQENASEYLAITSKENCCTGVQVAE 218  
 RESULT 11  
 Q8WU42 PRELIMINARY; PRT; 186 AA.  
 AC 08WU42;  
 DT 01-MAR-2002 (TRENBLREL. 20, Created)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
 DE SCN1B protein (Fragment).  
 GN Name=SCN1B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Caeavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley D.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Kidney;  
 RX Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC021266; AAH21266.2; -  
DR Pfam; PF00047; 1g; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
SQ SEQUENCE 186 AA; 21554 MW; A7DABF7E75FACF00 CRC64;

Query Match 37.6%; Score 423; DB 2; Length 186;  
Best Local Similarity 48.9%; Pred. No. 3e-30;  
Matches 91; Conservative 30; Mismatches 57; Indels 8; Gaps 5;

QY 38 GNPWKLRICSCMRKEEVEATTVEMFPRPGKDFL-IEYRNHGOVESP--FOGRLQW 94  
DB 1 GMFTKILICISCKRSEETAEFTETWTRQKTEEFVKILRYENNVQLBEDEREGRVW 60  
QY 95 NGS---KDLQDVSTTVANTLNDGLTYCNVSRFEFEARHPFKTRLLPLRTEAGE 151  
DB 61 NSGRGTQDLQDLSFTINVTYHNSGDYCHYRLLFENYEHNTSVVKKIIEVVQANR 120  
QY 152 DFTSVSEIMWYILVFLTWLILEMTYCYRKVSKA-EBAAGNADSYLAIPSENKEN-S 209  
DB 121 DAMSISEIMWYILVFLTWLILEMTYCYRKIAAETATAQENASBYLAITSEKENT 180  
QY 210 AVPEVE 215  
DB 181 GVOVAE 186

RESULT 12

Q9OXU3 PRELIMINARY; PRT; 273 AA.

ID Q9OXU3;  
AC Q9OXU3;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Voltage-gated sodium channel subunit beta1-A.  
GN Name=SCN1B;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN 1;  
RX SEQUENCE FROM N.A.  
RX MEDLINE=200952877; PubMed=10625649; DOI=10.1074/jbc.275.2.1079;  
RA Kazen-Gillespie K.A., Ragsdale D.S., D'Andrea M.R., Mattei L.N.,  
RT Rogers K.E., Isom L.L.;  
RT "Cloning, localization, and functional expression of sodium channel  
RT beta1a subunit";  
RL J. Biol. Chem. 275.1079-1088(2000).  
DR EMBL; AF182949; AAR25186.1; -  
DR GO; GO:0005216; F:ion channel activity; IEA.  
DR InterPro; IPR007110; IG-1like.  
DR Pfam; PF00047; 1g; 1.  
KW Ionic channel.  
SQ SEQUENCE 273 AA; 31063 MW; 156A31899A906849 CRC64;

Query Match 23.4%; Score 262.5; DB 2; Length 273;  
Best Local Similarity 39.3%; Pred. No. 1.6e-15;  
Matches 68; Conservative 23; Mismatches 53; Indels 29; Gaps 5;

QY 10 LALVLIWVSGPFCVPEPSETEAVQGNPMKLRICSCMRKEEVEATTVEMFPRREGG 69  
DB 5 LALVVGALVSSAGGCVEDSETEAVYGMFTKILICISCKRSEETAEFTETWTRQKGT 64  
QY 70 KDFL-IEYRNHGOVESP--FOGRLQWGS---KDLQDVSTTVANTLNDGLTYCNVS 123  
DB 65 EEFVKILRYENNVQLBEDEREGRVWNSRGKQDLQDLSFTINVTYHNSGDYCHY 124  
QY 124 REFEFEARHPFKTRLLPLRTEAGEFTSVSEIMWYIL---LVPLTLW 172  
DB 125 RLFFFDNY-----EHNTSVVKKIIEVVQKGSVLTW 158

RESULT 13

O6TN97

PRELIMINARY; PRT; 268 AA.

ID O6TN97;  
AC O6TN97;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Voltage gated sodium channel beta1b subunit.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 1;  
RX SEQUENCE FROM N.A.  
RX MEDLINE=22985127; PubMed=14622265;  
RA Qin N., D'Andrea M.R., Lubin M.U., Shafae N., Codd E.E., Correa A.M.;  
RT "Molecular cloning and functional expression of the human sodium  
RT channel beta1b subunit, a novel splicing variant of the beta1  
RT subunit";  
RL Eur. J. Biochem. 270.4762-4770(2003).  
DR EMBL; AY391842; AAR25552.1; -  
DR GO; GO:0005216; F:ion channel activity; IEA.  
DR InterPro; IPR007110; IG-1like.  
DR Pfam; PF00047; 1g; 1.  
KW Ionic channel.  
SQ SEQUENCE 268 AA; 30440 MW; D9A001E676C0FAD1 CRC64;

Query Match 23.0%; Score 258.5; DB 2; Length 268;  
Best Local Similarity 43.2%; Pred. No. 3.6e-15;  
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 10 LALVLIWVSGPFCVPEPSETEAVQGNPMKLRICSCMRKEEVEATTVEMFPRREGG 69  
DB 5 LALVVGALVSSAGGCVEDSETEAVYGMFTKILICISCKRSEETAEFTETWTRQKGT 64  
QY 70 KDFL-IEYRNHGOVESP--FOGRLQWGS---KDLQDVSTTVANTLNDGLTYCNVS 123  
DB 65 EEFVKILRYENNVQLBEDEREGRVWNSRGKQDLQDLSFTINVTYHNSGDYCHY 124  
QY 124 REFEFEARHPFKTRLLPLRTEAGE 151  
DB 125 RLFFFDNY-----EHNTSVVKKIIEVVQK-GE 151

RESULT 14

O6LE66

PRELIMINARY; PRT; 66 AA.

ID O6LE66;  
AC O6LE66;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Voltage-dependent Na+ channel beta-1 subunit (Fragment).  
GN Name=beta 1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN 1;  
RX SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX MEDLINE=96140573; PubMed=8549781; DOI=10.1016/0014-5793(95)01400-4;  
RA Dib-Hajj S.D., Waxman S.G.;  
RT "Genes encoding the beta 1 subunit of voltage-dependent Na+ channel in  
RT rat, mouse and human contain conserved introns";  
RL FEBS Lett. 377.485-488(1995).  
RN 12;  
RX SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX MEDLINE=92271207; PubMed=1375395;  
RA Isom L.L., De Jongh K.S., Patton D.E., Reber B.F., Offord J.,  
RA Charbonneau H., Walsh K., Goldin A.L., Caterall W.A.;  
RT "Primary structure and functional expression of the beta 1 subunit of  
RT the rat brain sodium channel.";

RL Science 256:839-842(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95024086; PubMed=7937931;  
RA Oh Y., Waxman S.G.;  
RT "The beta 1 subunit mRNA of the rat brain Na+ channel is expressed in  
RT glial cells."  
RL Proc. Natl. Acad. Sci. U.S.A. 91:9985-9989(1994).  
DR EMBL: L48688; AAB02428.1; -  
DR GO: GO:0005216; F-10n channel activity; IEA.  
KM Ionic channel.  
FT NON\_TER 1  
SQ SEQUENCE 66 AA; 7208 MW; 4DB598740914D95B CRC64;

Query Match 18.5%; Score 208; DB 2; Length 66;  
Best Local Similarity 63.6%; Pred. No. 2.8e-11;  
Matches 42; Conservative 12; Mismatches 10; Indels 2; Gaps 2;

QY 152 DFTSVSEIMMYTLVFLTMLLIEMICYRKVSKA-EEAQAENASDYLAIPSENKEN-S 209  
DB 1 DWASIVSEIMYVLIVLTLVLAENVYCYKKAATAEAQAENASEYLAITSSEKNCST 60

QY 210 AVPEEE 215  
DB 61 GVOVAE 66

RESULT 15

Q8JFG6 PRELIMINARY; PRT; 203 AA.  
AC Q8JFG6;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Myelin protein zero.  
GN Name=mpz;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Myelin;  
RA Schweitzer J., Becker T., Becker C.G., Schachner M.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL: AJ489219; CAD32961.1; -.  
DR HSSP; P06907; INED.  
DR ZFIN; ZDB-GENE-010724-4; mpz.  
DR GO: GO:0016020; C:membrane; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000920; Myelin\_P0.  
DR PRINTS; PR00213; MYELINP0.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
SQ SEQUENCE 203 AA; 22097 MW; 12614E9076D373D1 CRC64;

Query Match 15.9%; Score 178.5; DB 2; Length 203;  
Best Local Similarity 26.9%; Pred. No. 4.6e-08;  
Matches 53; Conservative 41; Mismatches 86; Indels 17; Gaps 7;

QY 10 LLSLTLIVWVSVPFCVSETPSETEAVQGNPKKLCISCMKREVEATVVEWFPYRPEG 69  
DB 7 LFSVVLGLIASQSTALVAVTDEKHALVGSIVRLSC-SFSSWQWTSPEVSTWHRYPDGA 65

QY 70 KDPL-IVERYNG--HOEVSPPQRLQWNGSKLDQVSITVNLVTLNDSGLTYCNVSRF 126  
DB 66 KDAISIFHHGGGEAVPANKGPFQNRLEFVGNPSRDSILIKNLDPGDNFTCDAKNPP 125

QY 127 EPEARPPVVKTRLLPL-RVTEBAGEFTSVSEIMMYTLV---FLTMLLIEMICY- 180  
DB 127 EPEARPPVVKTRLLPL-RVTEBAGEFTSVSEIMMYTLV---FLTMLLIEMICY- 180

DB 126 DIGH---PSTIRLLVEKVPVQAGVITGSIIGVVLGLLIIVAIYYIMRFLVARRVSL 182  
QY 181 ----YRKVSKAEBAQE 193  
DB 183 SMSKHGKKKGKGGSSQ 199

Search completed: March 31, 2005, 20:21:50  
Job time : 117 secs



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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 18:22:12 ; Search time 5660 Seconds  
(without alignments)  
10795.411 Million cell updates/sec

Title: US-09-977-579-4

Perfect score: 1261  
Sequence: 1 cccctccctccgcagctgagc.....tgcacagactgagagccgg 1261

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_ptg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1261	100.0	1261	6 AR359850	AR359850 Sequence
2	1261	100.0	1261	6 AX039100	AX039100 Sequence
3	1261	100.0	1261	6 HSAD23396	AJ243396 Homo sapi
4	909.4	72.1	5306	9 AB032984	AB032984 Homo sapi
5	835.8	66.3	3296	9 AB097521	AB097521 Macaca fa
6	592.4	47.0	606	6 C0728741	C0728741 Sequence
7	575.8	45.7	4169	10 BC053919	BC053919 Mus muscu
8	559.6	44.4	2632	6 AX048005	AX048005 Sequence
9	559.6	44.4	3107	10 AF378093	AF378093 Rattus no
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11	556.4	44.1	3910	10 BC070899	BC070899 Rattus no
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C	20	428	33.9	127347	2	AP000682	AP000682 Homo sapi
C	21	428	33.9	144833	2	AC063921	AC063921 Homo sapi
C	22	428	33.9	149800	2	AC021981	AC021981 Homo sapi
C	23	428	33.9	172546	2	AC024604	AC024604 Homo sapi
C	24	428	33.9	178169	9	AP002765	AP002765 Homo sapi
C	25	428	33.9	181471	9	AC069539	AC069539 Homo sapi
C	26	405	32.1	178431	2	AP002749	AP002749 Homo sapi
C	27	370.8	29.4	922	5	BX935227	BX935227 Gallus ga
C	28	334	26.5	912	5	BX931708	BX931708 Gallus ga
C	29	270.2	21.4	1654	5	BC077295	BC077295 Xenopus la
C	30	229.6	18.2	172546	2	AC024604	AC024604 Homo sapi
C	31	228	18.1	144833	2	AC063921	AC063921 Homo sapi
C	32	228	18.1	149800	2	AC021981	AC021981 Homo sapi
C	33	216	17.1	178431	2	AP002749	AP002749 Homo sapi
C	34	213	16.9	174285	2	AC145484	AC145484 Lemur cat
C	35	179	14.2	140307	2	AC135353	AC135353 Mus muscu
C	36	179	14.0	66980	2	AC148331	AC148331 Mus muscu
C	37	177	14.0	238861	2	AC013796	AC013796 Homo sapi
C	38	174.2	13.8	214306	2	AC128723	AC128723 Rattus no
C	39	148.2	11.8	657	4	OCU53382	UC5382 Oryctolagus
C	40	148.2	11.8	657	6	AX048005	AX048005 Sequence
C	41	145.4	11.5	1404	9	HUMSCN1BA	L10338 Human sodiu
C	42	143.8	11.4	617	6	CQ722293	CQ722293 Sequence
C	43	143.8	11.4	1335	9	HUMVWSC1B	I16242 Homo sapien
C	44	143.8	11.4	1525	9	BC067122	BC067122 Homo sapi
C	45	138.6	11.0	1125	10	MMU46681	U46681 Mus muscula

## ALIGNMENTS

RESULT 1	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
LOCUS	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
DEFINITION	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
ACCESSION	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
VERSION	AR359850.1	GI:33766660				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1261)					
AUTHORS	Healin P. and Lynnam N.R.					
TITLE	Vehicle interior rearview mirror assembly including an					
JOURNAL	accessory-containing housing					
FEATURES	Patent: US 6593565-A 4 15-JUL-2003;					
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Best Local Similarity	100.0%; Pred. No. 3.1e-288;					
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QY	61	AAGGTGAGTTCGCGGGTGGCGGGAGGAGGAGCTGTCGATGAGCGCGGAGGA	120			
DB	61	AAGGTGAGTTCGCGGGTGGCGGGAGGAGGAGCTGTCGATGAGCGCGGAGGA	120			
QY	121	GCAGGCGGAGCGGCTGATCGCTCCCTCGAAGTGGGAGGTCGATGAGGCTTAG	180			
DB	121	GCAGGCGGAGCGGCTGATCGCTCCCTCGAAGTGGGAGGTCGATGAGGCTTAG	180			
QY	181	GGCCCAAGCCCAAGCCGCTCCCAAAAGTCCCAAGGCTCCCGAGGACCGGTGCTG	240			
DB	181	GGCCCAAGCCCAAGCCGCTCCCAAAAGTCCCAAGGCTCCCGAGGACCGGTGCTG	240			
QY	241	GCCTTCCTTCGAGTCAAGAGTGGCCCTCGGGGAGGAGTTCGTCACCAAGGTTCTCG	300			

D	241	GCCCTTCTTGCGTACGAAAGTCCGCCCTCGGGGCACTTGTCGCCAAGAGGTTTCC	300
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Q	1021	TAGAACAGAGCAAGTGTGACATGAGTGGCTGAACACTGAGGAGCTGACATCCCATG	1080
D	1021	TAGAACAGAGCAAGTGTGACATGAGTGGCTGAACACTGAGGAGCTGACATCCCATG	1080
Q	1081	TTGAGCAATGTCAATGGATATGAGAGGGCGCCCAAGGGCCCAATCGCTTCCCTTCAATG	1140
D	1081	TTGAGCAATGTCAATGGATATGAGAGGGCGCCCAAGGGCCCAATCGCTTCCCTTCAATG	1140
Q	1141	ATCATATGTTCTGTTCACTTCAATCATACATCACTGCTGAGCTTTCACTCT	1200
D	1141	ATCATATGTTCTGTTCACTTCAATCATCACTGCTGAGCTTTCACTCT	1200
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D	1201	GACTCCCTAATCTCATAGACCTTACGACCATTAAGACTTGTGCCAAGCTGAGAAAGCG	1260
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D	1261	G 1261	

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 DB 721 GGCCTTACACCTGCAATGTGTCCCGGAGTTTGAAGGCGCATCGGCGCTTTGTG 780  
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 DB 781 AAGACGACGGGGTGATCCCGCTTAAGGTACCCGAGAGGCTGAGAGCACTTCACTCT 840  
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 DB 841 GTGGTCTCAGAAATCATGATGATCATCTTCTGTCTTCTTCTTCTCAACCTGTGCTGATC 900  
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 REFERENCE 1 Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K., Pinnock, R.D., Hynes, J., Richardson, P.J., Mizunuchi, K. and Jackson, A.P.  
 TITLE beta-3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)  
 MEDLINE 20160948  
 PUBMED 10688874  
 REFERENCE 2 Morgan, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM  
 REMARK Revised by [4]  
 REFERENCE 3 (bases 1 to 1261)

AUTHORS Morgan, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM  
 COMMENT On Mar 14, 2000 this sequence version replaced GI:7160974.  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases)  
 AUTHORS Hironaka, M., Nagase, T., Ishikawa, K., Kikuno, R., Nomura, N. and Ohara, O.  
 TITLE Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain  
 JOURNAL DNA Res. 6 (5), 329-336 (1999)  
 MEDLINE 10574461  
 PUBMED 10574461  
 REFERENCE 2 (bases 1 to 5306)

AUTHORS Ohara, O., Nagase, T. and Kikuno, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp, URL: http://www.kazusa.or.jp/huge/, Tel: +81-438-52-3913, Fax: +81-438-52-3914)

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DB	1 AGAAGATGCTGCCTTCAACAGATTGTTCCCTGCGTTCCTGCTTATCTACTCGGG 60
QY	431 TCAGTGTCTGTTCCCTGTGTGTGGAAAGGCCCTGGAGAAGAGGCGGTGAGGGCA 490
DB	61 CCAAGTGTCTTCCCGTGTGTGTGGAAAGGCCCTGGAGAAGAGGCTGTGAGGGCA 120
QY	491 ACCCATGAAGCTCGCTGCATCTCTGCAATGAAGAAGAGAGAGGTGGAGCCACCAAG 550
DB	121 ACCCATGAAGCTCGCTGCATCTCTGCAATGAAGAAGAGAGAGGTGGAGCCACCAAG 180
QY	551 TGTGTGAATGTTCTCAAGAGCCGAGAGGCGGTAAAGATTTCCTTAATTCAGATATGGA 610
DB	181 TGTGTGAATGTTCTCAAGAGCCGAGAGGCGGTAAAGATTTCCTTAATTCAGATATGGA 240
QY	611 ATGGCCACCGAGAGAGTGGAGAGCCCTTCAAGGGGGCCCTGCAGTGAATGGACGAAG 670
DB	241 ATGGCCACCGAGAGAGTGGAGAGCCCTTCAAGGGGGCCCTGCAGTGAATGGACGAAG 300
QY	671 ACCTCGAGAGAGGTTCATCACTGTGCTCAACGTCACTTGAAGCACTTGTGGCTTACA 730
DB	301 ACCTCGAGAGAGGTTCATCACTGTGCTCAACGTCACTTGAAGCACTTGTGGCTTACA 360
QY	731 CCTGCAATGTGTCCCGGAGAGTTTGAAGTTGAGGCGATCGGCCCTTTGTGAAGCAGCG 790
DB	361 CCTGCAATGTGTCCCGGAGAGTTTGAAGTTGAGGCGATCGGCCCTTTGTGAAGCAGCG 420
QY	791 GGCTGATCCCCCTTAAGAGTCAACGAGAGAGCTTGAAGAGACTTACCTCTGTGTCTCAG 850
DB	421 GGCTGATCCCCCTTAAGAGTCAACGAGAGAGCTTGAAGAGACTTACCTCTGTGTCTCAG 480
QY	851 AAATCATGATGTATCATCTCTGTGTTCTTCCCTCAACCTGTGGCTGCTATGAGATGAT 910
DB	481 AAATCATGATGTATCATCTCTGTGTTCTTCCCTCAATTTGTGGCTGCTATGAGATGAT 540
QY	911 ATTGCTACAGAAAGGTCTCAAAAGCCGAGAGAGGAGGCCCAAGAAAGCGCTTGTACTAC 970
DB	541 ATTGCTACAGAAAGGTCTCAAAAGCCGAGAGAGGAGGCCCAAGAAAGCGCTTGTACTAC 600
QY	971 TTGGCATCCCATCTGAGAACAGAGAACTTCTGCGGTACCAAGTGGAGAAATGAAACAGA 1030
DB	601 TTGGCATCCCATCTGAGAACAGAGAACTTCTGAGTACCAAGTGGAGAAATGAAACAGA 660
QY	1031 GCAGTGTGACATGAGGTGGCTGTGAACACTTGAGGGACTTGACATCCATGTTACGCAATG 1090
DB	661 GCAGTGTGACATGAGGTGGCTGTGAACACTTGAGGGACTTGACATCCATGTTACGCAATG 720
QY	1091 TCATATGACATCAGAGAGGAGCCCAAGAGGCCCATTCGCTTCCCTTCATGATCATCATTTGTT 1150

Db	721	TCATGCGATCAGAGGGGTGCCCCAAGGGTCCCATTTGATCCCTTCATGCATCATCTT	780
Qy	1151	CTGTTCAATTCATTCATCATATCATTCACCTGCTGCTTGAGCTTTCACTTGACCTCCCTAA	1210
Db	781	CT----ATTCAATTCATTCATCATACATGCACTGCTGCTTGAGCTTTCACTTGACCTCTTAA	836
Qy	1211	CTCCATCAGACCTCTTACGCACCATTAAGACTCTGCGACAGACTGAGAAGCC	1259
Db	837	CTCCATCAGACCTCTTACGTAACCATTAAGACTCTGCGACAGAACGAGAAGCC	885
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LOCUS	CQ728741	606 bp	DNA
DEFINITION	Sequence 14675 from Patent WO02068579.	linear	PAT 03-FEB-2004
ACCESSION	CQ728741		
VERSION	CQ728741.1	GI:42298386	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.		
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanecons or transcripts, for detecting expression and other uses thereof		
JOURNAL	Patent: WO 02068579-A 14675 06-SEP-2002;		
FEATURES	PE Corporation (NY) (US)		
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Best Local Similarity	99.8%;	Pred. No. 1,2e-129;	
Matches	593;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
Qy	430	GTCAAGTGTCTGCTTCCCTGCTGTGTGTGGAAGTGCCTCGAGACGAGAGCCGTGAGGGC	489
Db	13	GTCAAGTGTCTGCTTCCCTGCTGTGTGTGGAAGTGCCTCGAGACGAGAGCCGTGAGGGC	72
Qy	490	AAACCCATGAAGAGCTGCGCTGCACTTCCTCGCATGAAGAAGAGAGAGTGAAGCCACACAG	549
Db	73	AAACCCATGAAGAGCTGCGCTGCACTTCCTCGCATGAAGAAGAGAGAGTGAAGCCACACAG	132
Qy	550	GTGTGTGAATGGTTCTTACAGGCCCGAGAGCGGTAAAGATTTCTTATTTACAGATAGCG	609
Db	133	GTGTGTGAATGGTTCTTACAGGCCCGAGAGCGGTAAAGATTTCTTATTTACAGATAGCG	192
Qy	610	AATGGCCACACGAGAGGTGAGAGCCCTTTTACAGGGCGCTTGACATGTGAATGGACAGAG	669
Db	193	AATGGCCACACGAGAGGTGAGAGCCCTTTTACAGGGCGCTTGACATGTGAATGGACAGAG	252
Qy	670	GACCTGCAAGAGAGTGTCCATCATCATGTGTGCAACGTCACTTGAAAGCATCTGGGCTCTAC	729
Db	253	GACCTGCAAGAGAGTGTGTCCATCATCATGTGTGCAACGTCACTTGAAAGCATCTGGGCTCTAC	312
Qy	730	ACCTGCAATGTGTCCCGGAGATTGTTAGTTGAGGCGCATCGGCCCTTTGTGAAAGCAGAG	789
Db	313	ACCTGCAATGTGTCCCGGAGATTGTTAGTTGAGGCGCATCGGCCCTTTGTGAAAGCAGAG	372
Qy	790	CGGCTGATCCCTCTAAGAGTCAACGAGAGAGGTGAGAGAGACTTCACTTGTGTGTCTCA	849
Db	373	CGGCTGATCCCTCTAAGAGTCAACGAGAGAGGTGAGAGAGACTTCACTTGTGTGTCTCA	432
Qy	850	GAAATCATGATGTATATCTCTTGTGTTCTTCCCAACCTGTGGCTGCTCATGGAAGATGATA	909
Db	433	GAAATCATGATGTATATCTCTTGTGTTCTTCTTCACTTGTGTGCTGCTCATGGAAGATGATA	492

CY	910	TATGTCTAAGAAAGGTCCTCAAAGCCGAAGAGCACCACCAAGAAGAAAACGGCTCGACTAC	969
DB	493	TATTGTCAACGAAAGGTTCTCAAAGCCGAAGAGCACCACCAAGAAGAACGGCTTGACTAC	552
CY	970	CTTCCCATCTCCATCTGAGAACCAAGAGAACTCTGCCTGATCCAGTAGAGGATAATG	1023
DB	553	CTTCCCATCTCCATCTGAGAACCAAGAGAACTCTGCCTGATCCAGTAGAGGATAATG	606
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
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Query Match 45.7%; Score 575.8; DB 10; Length 4169;
Best Local Similarity 86.7%; Pred. No. 1,1e-125;
Matches 658; Conservative 0; Mismatches 97; Indels 4; Gaps 2;

QY 266 CCCCTGGGGGAGTTCCTCCAAAGGTTTCCTCGAAAGATCTGAGAGGCGCAGTCT 325
DB 202 CCTTAGGGGAGTAACTCCCTGAAGGTTCTCGAAAGATC-AGAGGGCTCAGTCT 259

QY 326 TGACCGAGGAATCTCTGTGTGAGCTTGGAAGCCGCGCCAGAAATGCTGCT 385
DB 260 TGACAA--GATCCTCTGTGTCAGTTCAGAAACCACTTACGAGAAAGATCCTGCT 317

QY 386 TCATAGATGTTCCCTCCGCTTCTCTGCTTATCTAAGGTCAGTCTGCTCC 445
DB 318 TCACAGATGTTCTCCCTAGCTTCTCTAGTCTCATCTAGGTCAGAGTCTGCTCC 377

QY 446 CTGTGTGTGGAAGTCCCTCGAGACGAGGCCGTGCAAGGCAACCCCATGAAGCTGC 505
DB 378 CTGTGTGTGGAAGTCCCTCGAGACGAGGCCGTGCAAGGCAATTCATGAAGCTGA 437

QY 506 GCTGCACTTCTCTGATGAGAGAGAGAGTGAAGCCACACGGTGTGGAATGTTCT 565
DB 438 GATGCACTTCTCTGATGAGAGAGAGAGTGAAGCCACACTGTAGTGAATGTTCT 497

QY 566 ACAGGCCCGAGGCGGTAAAGATTTCTTATTATGAGTATCGGAATGCGACACAGAGG 625
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QY 626 TGAAGACCCCTTTCAGGGCGCTGAGTGAATGAGCAAGACCTGCAAGACGTT 685
DB 558 TGAAGACCCCTTTCAGAGGTCGTCTGAGTGAATGAGCAAGACCTGCAAGACGTTAT 617

QY 686 CCATCACTGTGCTCAAGCTGCTGAAGCACTTGGCCCTTACACCTGCAATGTGTCC 745
DB 618 CCATCACTGTGCTCAAGCTGCTGAAGCACTTGGCCCTTACACATGTAATGTGTCCA 677

QY 746 GGAAGTTGAGTTGAGGCGCATCGGCCCTTGTGAAGAGACGCGGCTGATCCCTTAA 805
DB 678 GGAAGTTGAGTTGAGGCGCATCGGCCCTTGTGAAGAGACCAAGACTAATCCCTTGC 737

QY 806 GAGTCAACGAGAGGCTGAGAGAGACTTCACTCTGTGTCTGAGAAATCATGATGACA 865
DB 738 GAGTCACTGAAGAGGCGGAGAGAGACTTCACTCTCGTGTCTGAGAAATCATGATGACA 797

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QY 866 TCCTTCGTGCTTCTTCAACCTGTGGCTGCTCATGAGATGATATTTGCTACAGAAAG 925
DB 798 TCCTTCGTGCTTCTTCAACCTGTGGCTGCTCATGAGATGATATTTGCTACAGAAAG 857

QY 926 TCTCAAAAGCCGAAGAGGACGCCAAGAAACCGTCTGACTACTTGCATCCATCTG 985
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QY 986 AGAACAGAGGAATCTGCGGTGCTCAGTGAAGATGAA 1024
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RESULT 8
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LOCUS
DEFINITION
Sequence 22 from Patent WO0069912.
AX048005
ACCESSION
VERSION
AX048005.1 GI:11876883
KEYWORDS
SOURCE
ORGANISM
Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1
Curtis,R.A.
Gene encoding a sodium channel beta-3 subunit protein
Patent: WO 0069912-A 22 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

Query Match 44.4%; Score 559.6; DB 6; Length 2632;
Best Local Similarity 84.4%; Pred. No. 7.3e-122;
Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

QY 371 AGAAGATGCTGCTTCAATAGATGTTTCCCTGAGCTCTCGTCTATCTACGAG 430
DB 73 AAAAGATGCTGCTTCAATAGATGTTTCCCTGAGCTCTCGTCTATCTACGAG 132

QY 431 TCAGTGTGCTTCCCTGTGTGTGGAAGTCCCTCGAGACGAGGCCGTGCAAGGCA 490
DB 133 TCAGTGTGCTTCCCTGTGTGTGGAAGTCCCTCGAGACGAGGCCGTGCAAGGCA 192

QY 491 ACCCATGAAGCTGCGCTGATCTCTGCAATGAAGAGAGAGTGAAGGCCACACCG 550
DB 193 ATCCCATGAAGCTGAGTGTATCTCTGCAATGAAGAGAGTGAAGGCCACACCG 252

QY 551 TGGTGAATGTTCTTCAAGGCCCGAGGCGGTAAAGTTTCTTATTATGAGTATCGGA 610
DB 253 TGGTGAATGTTCTTCAAGGCCCGAGGCGGTAAAGTTTCTTATTATGAGTATCGGA 312

QY 611 ATGGCCACGAGAGTGAAGAGCCCTTTCAGGGCGCTGAGTGAATGAGCAAGG 670
DB 313 ATGGCCACGAGAGTGAAGAGCCCTTTCAGGGCGCTGAGTGAATGAGCAAGG 372

QY 671 ACTGCAAGAGCTGTGCTCATCTGTGCTCAAGCTCACTGAAAGACTGTGGCTTACA 730
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QY 731 CCGCAATGATGTCGAGGAGTTTGAATTTGAGGCGATGCGCCCTTGTGAAGACGAG 790
DB 433 CCGCAATGATGTCGAGGAGTTTGAATTTGAGGCGATGCGCCCTTGTGAAGACGAG 492

QY 791 GGTGTATCCCTTGAAGTTCACGAGAGGCTGAGAGACTTCACTCTGTGTCTAG 850
DB 493 GGTGTATCCCTTGAAGTTCACGAGAGGCTGAGAGACTTCACTCTGTGTCTAG 552

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OY	851	AAATCATATATACATCCCTTCGGCTTCCACACCTGTGGCTGTATCATGATATAT	910
Db	553	AAATCATATATATACATCCCTTCGGCTTCCACACCTGTGGCTGTATATGATGATCT	612
OY	911	ATTGCTACAGAAAGGCTCTCAAAAGCCGAGAGGCAGCCCAAGAAAAGCGCTGACTAC	970
Db	613	ATTGCTACAGAAAGGCTCTCTAAAGCCGAGAGGAGCAGCAAGAAAATGCGCTGACTAC	672
OY	971	TTGCGATCCCATCTGAGAAACAAGAGAACTCTGCGGCTACAGATGAGAGAAATAGAACA	1030
Db	673	TTGCTATCCCTTCAGAGAAACAAGAGAACTCTGTGTACTCTGTGAGAGAAAT-----AT	726
OY	1031	GCAAGTGACATGAGGTGGCTGAAACACCTGAGGAGATGACATCCATGTTACGACATG	1090
Db	727	GTTGGTGACATGAGGTGATCTG-AGTGCTAGAGGAGCTGAGATATCCCAAGTTGAGTATG	785
OY	1091	TCAATGGGATCAGAGAGGGGGCCCCAAGGGCCCCCATGCGTTCCTTCATGATCATCAT	1146
Db	786	CCAGCAATATACAGAAATGCCCCCAGGTGTCCCAACACATCCATCTTTTCTATTTGAT	841

RESULT	9
LOCUS	AF378093
DEFINITION	AF378093 Rattus norvegicus sodium channel beta 3 subunit (SCNB) mRNA,
ACCESSION	AF378093 complete cds.
VERSION	AF378093.1 GI:14165175
KEYWORDS	Rattus norvegicus (Norway rat)
SOURCE	

REFERENCE	1 (bases 1 to 3107)
AUTHORS	Qu, Y., Curtis, R., Lawson, D., Gilbride, K., Ge, P., Distefano P.S., Sliwos-Santiago, I., Catterall W.A. and Scherer, T.
TITLE	Differential modulation of sodium channel gating and persistent sodium currents by the beta1, beta2, and beta3 subunits
JOURNAL	Mol. Cell. Neurosci. 18 (5), 570-580 (2001)
MEDLINE	21919106
PMID	11922146
REFERENCE	2 (bases 1 to 3107)
AUTHORS	Curtis, R.
TITLE	Direct Submission
JOURNAL	Submitted (05-MAY-2001) Neurobiology, Millennium Pharmaceuticals Inc., 75 Sidney Street, Cambridge, MA 02139, USA

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source	location/Qualifiers
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CDS	77. .724

## ORIGIN

Query Match	44.4%;	Score 559.6;	DB 10;	Length 3107;
Best Local Similarity	84.4%;	Pred. No. 7.3e-122;		
Matches 655; Conservative	0;	Mismatches 114;	Indels 7;	Gaps 2;

OY	371	AGAAGATGCCGCTTCAATAGATATGTTTCCCTGCGCTTCTCGTCTATCTAC	CGG	430
Db	72	AAAAGATGCTGCTTCAACAGATGCTTCCCTAGCTTCTTAGTCTATCTACT	CGG	131
OY	431	TCAGTGTCTGCTTCCCTGTGTGTGTGGAAGTGTCCCTCGAAGCGAGGCGGT	CAGGCA	490
Db	132	TCAGAGTCTGCTTCCCTGTGTGTGTGGAAGTGTCCCTCGAGAGACAGAA	GCGGTCAAGGCA	191
OY	491	ACCCCAATGAAGCTGCGCGTGCATCTCCCTGCATGAAAGAGAGAGGTG	AGGCCACCA	550
Db	192	ATCCCAATGAAGCTGAGGTGCATCTCCCTGCATGAAAGAGAGAGGTG	AGGCCACCACTG	251
OY	551	TGTGTGAATGTTTCTACAGGCCCGGACCGGTAAAGATTTCTTATTTAC	AGATTCGA	610
Db	252	TGTGTGAATGTTTCTACAGGCCCGGACCGGTAAAGATTTCTTATTTAC	AGATTCGA	311
OY	611	ATGGCCACCAAGAGGTGAGAGCCCTTTCAAGGGGCGCTTCGACGTG	ATGACAGAGG	670
Db	312	ATGGCCACCAAGAGGTGAGAGCCCTTTCAAGGGGCGCTTCGACGTG	ATGAGGAATGGAGCAAG	371
OY	671	ACCTGCAGAGAGTGTCCATCACTGTGTCTCAACGTTCATCTGGAACG	ACTCTGGGCTTACA	730
Db	372	ACCTGCAGAGAGTGTTCATCACTGTGTCTCAACGTTCATCTGGAACG	ACTCTGGGCTTACA	431
OY	731	CCGTGCAATGTATCCCGGAGGTTTGAGTTTGAAGGCGCATCGGCCCT	TTGTAAGCAGCGC	790
Db	432	CATGCAATGTATCCCGGAGGTTTGAGTTTGAAGGCGCATCGGCCCT	TTGTAAGCAGCGA	491
OY	791	GGCTGATCCCTTAAGAGTACCCGAGAGGCGTGAAGAGACTTCACTGT	GGTCTCAG	850
Db	492	GACTGATACCTTTGGAGTCACTGGAAGGCGGGAAGAACTTCACTGT	GGTCTCAG	551
OY	851	AAATCATGATGTACATCTTGTGTCTTCTCACCTGTGTGCTGTATG	AGATGATAT	910
Db	552	AAATCATGATGTACATCTTGTGTCTTCTCACCTGTGTGCTGTATG	AGATGATAT	611
OY	911	ATTGCTCAGAAAGGTCTCAAAAGCGGAAGAGGAGCCCAAGAAAGCG	CTGTGATACC	970
Db	612	ATTGCTCAGAAAGGTCTTGAAGCGGAGAGGAGGAGCAAGAAATGCG	TTGATACC	671
OY	971	TTGCTATCCATCTGAGAGCAAGAGAACTCTGCGTACCAAGTGAAG	AATAGAACAGA	1030
Db	672	TTGCTATCTCTTCAGAGAAACAAGAGAACTGTGTGTACCTGTG	AGAAATTA-----AT	725
OY	1031	GCAGTGTGACATGAGGTGGCGCTGAACAACCTGAGGAGCTGACAT	CCCATGTTACGCAATG	1090
Db	726	GTGTGTGTGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	GT	784
OY	1091	TCATGTGCAATGAGAGGGGCGCCCAAGGGGCCCATGCGTTCCCT	TATGTGATCAT	1146
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LOCUS	AX047984	3108 bp	DNA
DEFINITION	Sequence 1 from Patent WO006912.		linear
ACCESSION	AX047984		
VERSION	AX047984.1	GI:11876881	
KEYWORDS			
SOURCE			
ORGANISM	Rattus sp.		
	Rattus sp.		

REFERENCE	1
AUTHORS	Curtis, R. A.
TITLE	Gene encoding a sodium channel beta-3 subunit protein
JOURNAL	Patent: WO 0069912-A 1 23-NOV-2000
FEATURES	Millennium Pharmaceuticals, Inc. (US)
SOURCE	Location/Qualifiers
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Query Match	44.4%;	Score 559.6;	DB 6	Length 3108;
Best Local Similarity	84.4%;	Pred. No. 7.3e-122;		
Matches 655; Conservative	0;	Mismatches 114;	Indels 7;	Gaps 2

QY	371	AGAAATACCCTGCTTCATATGATTTGTTTCCCTGGATCTCTCGTGTATCTACATGGG	430
Dp	73	AAAGATCCCTGCTTCAACAGATTGCTTCCCTGACCTTCTTAAGTCTCACTACATG	132
QY	431	TCAGTGTCTCTCCCTGTGTGTGTGGAAGTGCCTCTGGAGCGAGGCGGTGACGGCA	490
Dp	133	TCAGAGTGTGCTTCCCTGTGTGTGTGGAAGTGCCTCTGGAGCAAGAGCGGTGACGGCA	192
QY	491	ACCCATTAACCTGGGCTGCATCTCTCTCTCAATAAGAGAGAGGTGGAGGCAACACGG	550
Dp	193	ATCCCATTAACCTGGAGTGCATCTCTCTCAATGAAGAGAGAGGTGGAGGCAACACTG	252
QY	551	TGTTGGAATGTTTCAACAGCCCGAGGCGGTAAAGATTTCCTTAATTAACGATATCGA	610
Dp	253	TGTTGGAATGTTTCAACAGGCTTGAGGGCGGTAAAGATTTCCTTAATTAATGATATCGA	312
QY	611	ATGGCCACACAGAGGTGAGAGGCCCTTTCAAGGGCGGCTCGAGTGAATGGCACAGG	670
Dp	313	ATGGCCACACAGGAAGTGAAGAGGCCCTTTCAAGGGCGGCTCGAGTGAATGGAGCAAG	372
QY	671	ACCTGCAGAGAGTGTTCATCACTGTGTCTCAAGTCACTGTGAAGCATCTGGCCCTTACA	730
Dp	373	ACCTGCAGAGAGGTATCCATCACTGTACTCAATGTCACTTGTGAATACCTGGCCCTTACA	432
QY	731	CCTGCAATGTGTCCCGGGAGTTTGAAGTTCGAGCCATCGGCCCTTTGTAAGACGAGGC	790
Dp	433	CATGCATGTGTCCAGGAGTTTCGAATTCGAGGCCACAGGCCCTTTTGTGAAGACGAGCA	492
QY	791	GAGTGATCCCCCTTAAGAGTCAACGAGAGGCTGAGAGGACTTCACTCTGTGTCTCAG	850
Dp	493	GACTGATACCTTTGGAGTCACTGTAAGAGGCGGAGGAAGACTTCACTCTCGTGTCTGG	552
QY	851	AAATCATATATGTAATCTCTTGTGTCTTCTCAACCTGTGCTGCTCATCGAATGATAT	910
Dp	553	AAATCATATATATATCTCTCTGTGTCTTCTCAACCTGTGCTGCTTATTTGAGATGATCT	612
QY	911	ATTGTCAAGAAAGGTCTCAAAAGCCGAAGAGGCAAGCCCAAGAAAGCGTGTGACTAC	970
Dp	613	ATTGTCAAGAAAGGTCTCTTAAGCCGAAGAGGCAAGCAAGAAATGTGTGTGACTAC	672
QY	971	TTGGCATCCATCTTGAGAACAGAGAACTCTGCGGTACAGATGAGAGAAATGAAACAGAA	1030
Dp	673	TTGGCATCCCTTCAAGAGAACAGAGAACTCTGTGTGTACTGTGAGGAAATA-----AT	726
QY	1031	GCAGTGTGACATGAGGTGGCTGAACACTGAGGGACTGGACATTCATGTTCAAGCAATG	1090
Dp	727	GTTGTGTGACATTTGAGGTATCTG-AGTGTGAGGGACTGGATATCCCAAGTTCAAGTATG	785
QY	1091	TCATATGGCATAGGAGGGGGCCCCAAGGGCCCCATCGCTCTCCCTCATGATTCAT	1146
Dp	786	CCAGCAATATACAGGAAGTGGCCCCAGGTGTCCCAACACATTCATCTTTTATTCAT	841

RESULT	11
LOCUS	BC070899
DEFINITION	BC070899 3910 bp mRNA linear ROD 28-SEP-2004
ACCESSION	Rattus norvegicus sodium channel, voltage-gated, type III, beta,
VERSION	mRNA (cDNA clone MGC:91409 IMG 67100476), complete cds.
KEYWORDS	BC070899
SOURCE	BC070899.1 GI:47477789
ORGANISM	MGC. Rattus norvegicus (Norway rat) Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS

TITLE	JOURNAL	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL
-------	---------	--------	-----------	---------	-------	---------

REMARK  
COMMENT

REFERENCE AUTHORS	JOURNAL PUBLISHED AUTHORS TITLE	REMARK COMMENT
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
1. (bases 1 to 3910) Strausberg, R.L., Collins, E.A., Grouse, L.H., Derze, J.G., Klauser, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapelton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schneitz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McEwan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Moley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulys, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Nadeau, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shchepankov, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. 2004 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
	12477932 2 (bases 1 to 3910) Director MGC Project.	
	Submitted (17-MAY-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgabs-rc@mail.nih.gov">cgabs-rc@mail.nih.gov</a> Tissue Procurement: Howard Jacobs cDNA Library Preparation: The I.M.A.G.E. Consortium (LNLN) cDNA Library Arrayed by: Express Genomics DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc.mgc@nhgri.nih.gov">nisc.mgc@nhgri.nih.gov</a> Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>	
	Ahtler, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Mastello, C., Makkeri, B., Mastriani, S.D., McCloskey, J.C., McGowan, J.J., Pearson, R., Statuttop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Series: IRAP kit: 175 Row: 9 Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 47575878. Location/Qualifiers	

gene

CDS

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Query Match	44.1%;	Score 556.4;	DB 10;	Length 3910;
Best Local Similarity	84.1%;	Pred. No. 4.2e-121;		
Matches 653;	Conservative	0;	Mismatches 116;	Indels 7;
				Gaps 2;

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Db	433	TCAGAGTCTGCTTCCCTGTGTGTGTGAAGTACCTCGAAGACAGAAACGGGTGACGGGTA	492
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Db	553	TGGTGAATGGTTCACAGAGCCCTGAGGGCGGTAAAGATTTTCTTATATATAGATTCGGA	612
OY	611	ATGGCCACAGAGAGGTGAGAGCCCTTTCAGGGGCGCTCAGTGAATGAGCAGAGAG	670
Db	613	ATGGCCACAGAGAGGTGAGAGCCCTTTCAGAGCCGTCTGACGTGAATGAGAGCAAG	672
OY	671	ACCTGCAGAGAGGTGTCCATCACTGTGTCTCAACGTACATCTGTGAACATCTGTGGCTCTACA	730
Db	673	ACCTGCAGAGAGGTATCCATCACTGATCACTCAATGTCACTTAAATGACTCTGTGGCTCTACA	732
OY	731	CCTGCAATGTGTCCCCGGGAGTTTGATTTGAAGGCGCATCGGCCCTTTGTGAAGACGACG	790
Db	733	CATGCAATGTGTCCAGGAGATTTCGAAATTCGAGGACACAGAGCCTTTTGTGAAGACGACGA	792
OY	791	GCGTGATCCCGCTTAAGAGTCAACCGAGAGGCGTGAAGAGACTTCACTCTGTGTCTCAG	850
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Db	853	AAATCATGATGTACATCCTTCTGTGTCTTCTCTCAACCTGTGGCTGTTTATGAGATGATCT	912
OY	911	ATTGTGTAAGAAAGGTCTCAAAAGCCGGAAGAGGCGCCCAAGAAAGCGGTCTGACTAC	970
Db	913	ATTGTGTAAGAAAGGTCTCTTAAAGCCGGAAGAGGCGCACAGGAAATACGTCTGACTAC	972
OY	971	TTGCCATCCCATCTGTAGAACAGAGAGAACTGTGCGGTACAGATGAGAGAAATATGAACAGGA	1030
Db	973	TTGCGATCCCTTTCAGAGAAACAGAGAGAACTGTGTGTACCTGTGAGAGAAAT-----AT	1028
OY	1031	GCAGTGTGACATGAGTGGGCTGTGAACACCTGAGGACTGTGACATCCATGTTTCAGCAATG	1090
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OY	1091	TCATATGAGATCAGAGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCAATGATCATAT	1146
Db	1086	CCAGCAATATACAGAGAGTGGCCCAAGGTATCCCAACACATTCATCTTTCTATATCAT	1141

RESULT 12	4025 bp	mRNA	linear	ROD 28-JUL-2004
AK173115				
LOCUS				
AK173115				

DEFINITION	Mus musculus mRNA for mKIAA1158 protein.
ACCESSION	AK173115
VERSION	AK173115.1 GI:50510814
KEYWORDS	FLI_CDNA.
SOURCE	Mus musculus (house mouse)

REFERENCE  
1  
Okazaki, N., Kikuno, R.F., Ohara, R., Inamoto, S., Koseki, H., ...  
AUTHORS

**TITLE**  
Prediction of the Coding Sequences of Mouse Homologues of KIAA

JOURNAL DNA Res. 11, 205-218 (2004)  
 REFERENCE 2 (bases 1 to 4025)  
 AUTHORS Okazaki, N., Kikuno, R.F., Nagase, T., Ohara, O. and Koga, H.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research

COMMENT  
(E-mail: mouse@kazusa.or.jp, Tel.: 81-438-52-3919, Fax: 81-438-52-3918)  
The CREATE program supported by Japan science and technology  
corporation; cDNA full insert sequencing: Kazusa DNA Research  
Institute; cDNA library construction, clone selection and 5'- &  
3'-end one pass sequencing.

FEATURES	Location/Qualifiers
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ORIGIN

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QY	409	TCTCTCGTCTTATCTATCTGGGTCAAGTCTGCTTCCCTGTGTGTGGAAAGTCCCTCG	468
Db	323	TCTTAACTGTCATCTACTGGGTCAAGTCTGCTTCCCTGTGTGTAGAAAGTACCTTCG	382
QY	469	GAGACGGAGGCCGTCGAGGGCAACCCCATGAAAGTGGCGTCAGTCTCTCGATGAAGAGA	528
Db	383	GAGACAGAGGCCGTCGAGGGCAATTCATGAGCTGAGATGATCTCTCTGATGAAGAGG	442

QY	529	GAGGAGGTGGAGG	CACCA	CGGTGTGTA	TGTTCTA	CAGGCTCCAGGGCGGTA	588
Db	443	GAGGAGGTGGAGG	CACCA	CTGTGTGAGTGGTTCTA	CAGGCTGAGGGCGGTA	AAGAT	502

QY	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL
589	TTCCCTATTACAGATTCGGAATGGCCACGAGAGGTGAGAGAGCCCTTTCAGGGGCGC	4176 bp mRNA linear ROD 08-OCT-2003	BC058636	1			Mus musculus	1	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Viallon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Valle, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.B., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	human and mouse cDNA sequences	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	22388257	2	(bases 1 to 4176)	Strausberg, R.	Direct Submission	Submitted (22-SEP-2003) National Institutes of Health, Mammalian

REMARK  
COMMENT

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA.

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk  
Email: [cgabs-rc@mail.nih.gov](mailto:cgabs-rc@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI)

DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.

Web site: <http://genome.iowa.edu>

Contact: [bento-soares@iowa.edu](mailto:bento-soares@iowa.edu); [tom-casavant@iowa.edu](mailto:tom-casavant@iowa.edu)

Bonaldi, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: <http://image.lnl.gov>

Series: Plate: Row: Column: 0

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23943798.

Location/Qualifiers

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1. 4176

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412. 1059

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547. 777

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ORIGIN

Query Match 43.0%; Score 542.6; DB 10; Length 4176;

Best Local Similarity 88.2%; Pred. No. 7.9e-118;

Matches 590; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

misc\_feature

QY 356 GAAGCCGCCAGCCGACGAGAGATGCTGCTCAATAGATTGTTCCCTGCTTCTTCG 415

DB 392 GAACCACTTACAGAAATATCCCTGCTTCAACAGATTGCTCCCTAGCTTCTTAG 451

QY 416 TGCTTCTTCTAGTGGTCAAGTGTGCTGCTCCCTGTGTGTGAAGTGCCTCGAGACG 475

DB 452 TGCTCATCTACTGGGTCAAGTGTGCTGCTTCTGTGTGTGAAGTGCCTCGAGACG 511

QY 476 AGCCGTCAGAGGCAACCCCATGAAGCTGCTGCTTCTTCATGAAGAGAGAGAGG 535

DB 512 AACCCGTCAGAGGCAATTCATGAAGCTGATGATGATGATGATGATGATGATGATG 571

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Db	752	ACTCTGGCCTCTACATGTATGTGTCCAGGAGATTGAGTTGAAACACACGGGCCCT	811
QY	776	TTTGAAACAGACGGGGCTGATCCGCCCTTAAAGTACCGAGAGAGGCTGAGACACTTCA	835
Db	812	TTTGAAACAGCAAGACTTAATACCCCTGCGAGTCACTGAAGAGGGCGGAGAAAGCTTCA	871
QY	836	CCTCTGTGTCTCAGAAATTCATGATGTACATCTCTTGTCTTCTCTCACCCCTGTGGCTGC	895
Db	872	CCTCGTGTGTCTCGAATTCATGATGTACATCTCTGTCTTCTCTCACCTGTGGCTGT	931
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QY	1016	AGGAATAGA 1024	
Db	1052	AGGAATAA 1060	

RESULT	14
LOCUS	AY049036
DEFINITION	AY049036 670 bp mRNA linear ROD 01-OCT-2001
ACCESSION	Mus musculus brain and heart sodium channel beta 3 subunit mRNA,
VERSION	complete cds.
KEYWORDS	AY049036 AY049036.1 GI:15822811
SOURCE	.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eutharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	Chen, C., Avery, C., Kazen-Gillespie, K. and Isom, L.L.
REFERENCE	Mouse brain and heart beta 3 sodium channel cDNA
AUTHORS	Unpublished
TITLE	2 (bases 1 to 670)
JOURNAL	Chen, C., Avery, C., Kazen-Gillespie, K. and Isom, L.L.
REFERENCE	Direct Submission
AUTHORS	Submitted (30-JUN-2001) Pharmacology, University of Michigan, 1301
TITLE	MSRB III, Box 0632, Ann Arbor, MI 48109-0632, USA
JOURNAL	Location/Qualifiers
FEATURES	1..670
SOURCE	

CDS

[illegible]

ORIGIN

Query Match	42.9%	Score 540.6;	DB 10;	Length 670;
Best Local Similarity	89.3%	Pred. No. 2.4e-117;		
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Db	73	TCAGAGTCTGCTTCCCTGTGTGTGTAGAAAGTACCCTCGAGACAGAACCCGTGCAGGCGCA	132
OY	491	ACCCATGAACCTGCGCTGCATCTCCGCAATGAAGAAGAGAGAGTGAGGCGACCAAG	550
Db	133	ATTCCTAGAACCTAGATGATCTCTCTGCAATGAAGAAGAGAGAGTGAGGCGACCACTG	192
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Db	313	ACCTGAGGAGGTATTCATCTGTTCTTCAATGTCACTCTGAATGACTCTGAGCCTTCA	372
OY	731	CCTGCAATGTGTCCCGGAGTTTGAAGTTGAAGCGCATCGGCCCTTTGTGAAGACGAGC	790
Db	373	CATGTAATGTGTCCAGGGAGTTTGAGTTGAAAGCACACCGGCCCTTTGTGAAGACACAA	432
OY	791	GGCTGATCCCCCTTAAGATCAACGAGAGGCTGAGAGAGACTTCAACCTCTGTGTCTGAG	850
Db	433	GACTAATAATCCCTCGAGTCACTGAAGAGGCGGGAGAACTTCACTCCGCGGTCTGG	492
OY	851	AAATCATGATGTACATCTTCTGTGCTTCTCAACCTGTGCTGCTCATCGAGATGATAT	910
Db	493	AAATCATGATGTACATCTTCTGTGCTTCTCAACCTGTGCTGCTTATAGATGATCT	552
OY	911	ATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGCGACCCAGAAAGAACGCGTCTGACTAC	970
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OY	971	TTGCAATCCCATCTGAGAACAGAGGAACCTCGGCGTATCGATGGAGGAAT	1022
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## RESULT 15

LOCUS	AR359649	2220 bp	DNA	linear	PAT 17-AUG-2000
DEFINITION	Sequence 3 from patent US 6593565.				

## KEYWORDS

**SOURCE** Unknown

ORGANISM Unknown

**Unclass:**

REFERENCE 1 (bases 1 to 2220)

**AUTHORS** Heslin, P. and Lynam, N.R.

TITLE Vehicle interior rearview mirror assembly including an

accessory-containing housing

JOURNAL Patent: US 6593565-A 3 15-JUL-2003;

<b>FEATURES</b>	<b>Location/Qualifiers</b>
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## OPTICIN

Query Match 42.8%; Score 540; DB 6; Length 2220;

Best Local Similarity 89.3%; Pred. No. 3.3e-117;  
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QY 371 AGAAGATGCTGCTGCTTCAATAGATTGTTTCCCTGCTTCTCTGCTTACTACTGG 430
Db 358 AAAAGATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTCTCATCTACTGG 417
QY 431 TCAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
Db 418 TCAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
QY 491 ACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
Db 478 ATCCCATGAAGCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
QY 551 TGGTGAATGCTTCTACAGGCGGAGGCGGTAAGATTCTTATTATTAAGATGGA 610
Db 538 TGGTGAATGCTTCTACAGGCGGAGGCGGTAAGATTCTTATTATTAAGATGGA 597
QY 611 ATGGCCACGAGGAGTGGAGAGCCCTTTCAGGGGCGCTGAGTGAATGGCAGAG 670
Db 598 ATGGCCACGAGGAGTGGAGAGCCCTTTCAGGGGCGCTGAGTGAATGGCAGAG 657
QY 671 ACCTGAGAGAGTGTCCATCATGTGCTCAACGTCACTTGAACGACTGCTGCTTACA 730
Db 658 ACCTGAGAGAGTGTCCATCATGTGCTCAACGTCACTTGAACGACTGCTGCTTACA 717
QY 731 CTTGCAATGTGTCCCGGAGTTGAGTTGAGGCGCATCGCCCTTTGTGAAGAGAGC 790
Db 718 CATGCAATGTGTCCCGGAGTTGAGTTGAGGCGCATCGCCCTTTGTGAAGAGAGC 777
QY 791 GGTGATCCCTTAAGATGACCGAGAGGCTGGAGAGAGCTTCACTGCTGCTGCTCAG 850
Db 778 GACTGATACCTTTGCGAGTCACTGAGAGGCGGAGAGAGCTTCACTGCTGCTGCTCAG 837
QY 851 AAATCATGATGATCATCTCTTCTGCTTCTCTCAACCTGCTGCTGCTCATGAGTGAAT 910
Db 838 AAATCATGATGATCATCTCTGCTTCTCTCAACCTGCTGCTGCTCATGAGTGAAT 897
QY 911 ATTGCTACAGAAAGTCTCAAAAAGCGAGAGGAGCGCAAGAAACGCGTCTGACTACC 970
Db 898 ATTGCTACAGAAAGTCTCTTAAGGCGGAGAGGAGCGCAAGAAATGCGTCTGACTACC 957
QY 971 TTGCGCATCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 1022
Db 958 TTGCTATCCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 1009

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Search completed: April 1, 2005, 20:37:25  
Job time : 5670 secs

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CC The invention relates to a recombinantly expressed and isolated human  
CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally  
CC incorporated into a cell, is used to screen for specific modulators,  
CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,  
CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic  
CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,  
CC motor endplate diseases, hypertension, congestive heart failure and  
CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic  
CC and metastatic cancer cell lines). These activities can also be provided  
CC by gene therapy vectors that express (I) or the modulators. The  
CC modulators, also antibodies directed against (I), are used to detect  
CC sodium channel polypeptides. The present sequence represents a human  
CC SCN1B protein encoding cDNA

XX Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 1261; DB 10; Length 1261;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCCCTCCGAGCTGAGCTTACCTCGGCGCAAGAGCGAGGCGCGGAGTGG 60  
DB 1 CCTCTCCCTCCGAGCTGAGCTTACCTCGGCGCAAGAGCGAGGCGCGGAGTGG 60  
QY 61 AAGCTGAGTTCGCGGGGTGGGCGGAGCGAGCTGCTGCTGCTGAGCGCGGAGAGA 120  
DB 61 AAGCTGAGTTCGCGGGGTGGGCGGAGCGAGCTGCTGCTGCTGAGCGCGGAGAGA 120  
QY 121 GCGGGCGCGGAGCGGCTGATCGGCTCCCTCGAAGTGGGAGAGTCACTGAGGCTTAA 180  
DB 121 GCGGGCGCGGAGCGGCTGATCGGCTCCCTCGAAGTGGGAGAGTCACTGAGGCTTAA 180  
QY 181 GGGCCAAAGGCGCCCAAGGCTCCCAAGGCTCCCGAGGAGCCGAGTGTCTG 240  
DB 181 GGGCCAAAGGCGCCCAAGGCTCCCAAGGCTCCCGAGGAGCCGAGTGTCTG 240  
QY 241 GCGCTTCTCGGTCAGAAAGTGGCGCCCTGGGGGCGAGTTCGTCGCAAGAGGTTTCTCTG 300  
DB 241 GCGCTTCTCGGTCAGAAAGTGGCGCCCTGGGGGCGAGTTCGTCGCAAGAGGTTTCTCTG 300  
QY 301 AAGAAATCTGAGAGGGGCGAGTCTTGACCGAGGAATCTCTGTGTAGCCTTGAAGC 360  
DB 301 AAGAAATCTGAGAGGGGCGAGTCTTGACCGAGGAATCTCTGTGTAGCCTTGAAGC 360  
QY 361 GCGCAGCGCCCAAGAGTCTGCTTCAATGATTTGTTTCCCTGCTTCTGCTGCTT 420  
DB 361 GCGCAGCGCCCAAGAGTCTGCTTCAATGATTTGTTTCCCTGCTTCTGCTGCTT 420  
QY 421 ATCTAGTGGGTGAGTGTCTGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
DB 421 ATCTAGTGGGTGAGTGTCTGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 GTGCAAGGCGCAAGCCATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
DB 481 GTGCAAGGCGCAAGCCATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
QY 541 GCGCAGCGCCCAAGAGTCTGCTTCAATGATTTGTTTCCCTGCTTCTGCTGCTT 600  
DB 541 GCGCAGCGCCCAAGAGTCTGCTTCAATGATTTGTTTCCCTGCTTCTGCTGCTT 600  
QY 601 GAGTATCGGATGCGCAGAGAGTGAAGAGCCCTTTGAGGGGCGCTGAGTGAAT 660  
DB 601 GAGTATCGGATGCGCAGAGAGTGAAGAGCCCTTTGAGGGGCGCTGAGTGAAT 660  
QY 661 GCGCAGCGCCCAAGAGTCTGCTTCAATGATTTGTTTCCCTGCTTCTGCTGCTT 720  
DB 661 GCGCAGCGCCCAAGAGTCTGCTTCAATGATTTGTTTCCCTGCTTCTGCTGCTT 720  
QY 721 GCGCTTCTGAGCTGCAATGTGTCTGCGGAGTTTGAAGTGAAGTGGCGCTTGTG 780  
DB 721 GCGCTTCTGAGCTGCAATGTGTCTGCGGAGTTTGAAGTGAAGTGGCGCTTGTG 780  
QY 781 AAGACGACGGGGTGAATCCCTTAAGAGTCAACGAGAGGCTGAGAGGACTTCACTCT 840

DB 781 AAGACGACGGGGTGAATCCCTTAAGAGTCAACGAGAGGCTGAGAGGACTTCACTCT 840  
QY 841 GTGCTCAGAAATCATGATGTATCTCTTGTGTCTTCTCTCAACCTGTGGCTGTATC 900  
DB 841 GTGCTCAGAAATCATGATGTATCTCTTGTGTGTCTTCTCTCAACCTGTGGCTGTATC 900  
QY 901 GAGATGATATATGTCTACAGAAAGTCTCAAAAGCGGAGAGGCGCCCAAGAAAGCG 960  
DB 901 GAGATGATATATGTCTACAGAAAGTCTCAAAAGCGGAGAGGCGCCCAAGAAAGCG 960  
QY 961 TCTGACTACCTTCCATCCCATCTGAGAACAGAGAACTCTCGGTACCATGAGAGAA 1020  
DB 961 TCTGACTACCTTCCATCCCATCTGAGAACAGAGAACTCTCGGTACCATGAGAGAA 1020  
QY 1021 TAGAAGCAGAGCAGTGTGATGATGAGTGGCTTGAACCTGAGAGGAGTCACTCCATG 1080  
DB 1021 TAGAAGCAGAGCAGTGTGATGATGAGTGGCTTGAACCTGAGAGGAGTCACTCCATG 1080  
QY 1081 TTGAGCAATGTCAATGGCATCAGAGGGGCGCCCAAGGGCGCCGCTTCCCTCATGC 1140  
DB 1081 TTGAGCAATGTCAATGGCATCAGAGGGGCGCCCAAGGGCGCCGCTTCCCTCATGC 1140  
QY 1141 ATCCATTTGTTCTGTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200  
DB 1141 ATCCATTTGTTCTGTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200  
QY 1201 GACTCCCTAATCTCATACAGCTCTTACGACCATTAAGACTTTCGACGAACTGAGAGCCG 1260  
DB 1201 GACTCCCTAATCTCATACAGCTCTTACGACCATTAAGACTTTCGACGAACTGAGAGCCG 1260  
QY 1261 G 1261  
DB 1261 G 1261

RESULT 3  
ADB78651  
ID ADB78651 standard; cDNA; 1261 BP.  
XX  
AC ADB78651;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human ion channel subunit cDNA mutant SCN1A exon 1 SEQ ID NO:22.  
XX  
KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;  
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antidiabetic;  
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;  
KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;  
KW ion channel dysfunction; human.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN NO2003008574-A1.  
XX  
PD 30-JAN-2003.  
XX  
PF 08-JUL-2002; 2002MO-AU000910.  
XX  
PR 18-JUL-2001; 2001AU-00006452.  
PR 05-MAR-2002; 2002AU-0000910.  
PR 13-MAY-2002; 2002AU-00002292.  
XX  
PA (BION-) BIONOMICS LTD.  
PA (WALL/) WALLACE R W.  
XX  
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;  
PI Berkovic SF, Scheffer IE;  
XX  
DR WPL; 2003-23932/23.  
XX

PT Identifying predisposition to an ion channel dysfunction, such as PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease, PT schizophrenia, anxiety and depression, by detecting encoding-gene PT mutation events.

Claim 6; SEQ ID NO 22; 106bp; English.

The invention relates to a novel method for identifying a subject predisposed to a disorder associated with ion channel dysfunction. The method comprises ascertaining if at least one of the genes encoding ion channel subunits (ICs) has undergone a mutation event so that a cDNA derived from the subject has any of 134 nucleotide sequences. The method of the invention has neurotropic, neuroprotective, inotropic, antipretic, antiarrhythmic, antimigraine, antidepressant, antiparkinsonian, neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and ophthalmological activity. A polynucleotide of the invention acts as an ion channel agonist, or ion channel antagonist. The methods, isolated nucleic acids, polypeptides, antibody, selective agonist, antagonist or modulator of an ion channel, cells and genetically modified non-human animal, are useful for the diagnosis and treatment of epilepsy and/or a disorder associated with ion channel dysfunction, such as hyper- or hypokalemic periodic paralysis, myotonia, malignant hyperthermia, myaesthesia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hypernatraemic hypoglycaemia of infancy, cystic fibrosis, congenital stationary night blindness and total colour blindness. The present sequence represents a mutant cDNA of the invention. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from Wipo at [http://wipo.int/publ/published\\_pat\\_sequences](http://wipo.int/publ/published_pat_sequences).

Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

99.9%; Score 1259.4; DB 10; Length 1261;

atches 1260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	CCCTCCCTTCCGAGCTGAGCTTAACTACCTGGGGCGCAAAACGACGAGGACAGGGCGGAGTGG	60
Db	1	CCCTCCCTTCCGAGCTGAGCTTAACTCTGGGGCGCAAAACGACGAGGACAGGGCGGAGTGG	60
QY	61	AAGCTGAGATTCCGGGGTGGGGGCGGAGGCGACTGTGCTGGTGTGAGCGCCGCGCAGA	120
Db	61	AAGCTGAGATTCCGGGGTGGGGGCGGAGGCGACTGTCCGTGGTGTGAGCGCCGCGCAGA	120
QY	121	GCGGGGCGCGGAGGCGGCTGATCGGCTTCCTCGAACTGGGGAGGTCCAGTGGGGTGCCTTAG	180
Db	121	GCGGGGCGCGGAGGCGGCTGATCGGCTTCCTCGAACTGGGGAGGTCCAGTGGGGTGCCTTAG	180
QY	181	GGCGCCAAAGCCCCACCGGCTCCAAAGCTCCCAAGGGCCCTCCCGAGGCAACGGGTGCTCG	240
Db	181	GGCGCCAAAGCCCCACCGGCTCCCAAAAGCTCCCAAGGGCCCTCCCGAGGCAACGGGTGCTCG	240
QY	241	GCCCTTCCTTCGGTCAAGAAAGTCGCCCCCTGGGGGCAAGTTCGTCGCAAGAGGTTTCTCG	300
Db	241	GCCCTTCCTTCGGTCAAGAAAGTCGCCCCCTGGGGGCAAGTTCGTCGTCGCAAGAGGTTTCTCG	300
QY	301	AAAGAACTTGAGAGGGCGCAGTTCCTTGAACGAGGGAATCTCTGTGTAGCTTGTGAAGC	360
Db	301	AAAGAACTTGAGAGGGCGCAGTTCCTTGAACGAGGGAATCTCTGTGTAGCCTTGTGAAGC	360
QY	361	CGCGACCCCCAGAAAGATGCTGCTTCAATAATTGTTTCCCTCGGCTTCTCTGTGCTT	420
Db	361	CGCGACCCCCAGAAAGATGCTGCTTCAATAATTGTTTCCCTCGGCTTCTCTGTGCTT	420
QY	421	ATCTACTGGGTGAGTGTCTGTCTCCCTGTGTGTGGAAGTGCCTCGAGACGGAAGCC	480
Db	421	ATCTACTGGGTGAGTGTCTGTCTCCCTGTGTGTGGAAGTGCCTCGGAACGGAAGCC	480
QY	481	GTGCAGGGCAACCCCAATGAAGCTGGCTGCAATCTCTGCATGAAGAGAGAGAGTGGAG	540

Db	481	GTGCAGGGCAACCCCATGAAGCTCGCTGCATCTCTGCATGAAGAGAGAGAGGTGAG	540
Qy	541	GCCACCAACGGTGTGGAATGGTTCTAAGGCCCGAAGGGCGGTAAAGATTCTTATTAC	600
Db	541	GCCACCAACGGTGTGGAATGGTTCTTACAGGCCCGAAGGGCGGTAAAGATTCTTATTAC	600
Qy	601	GAGATCGGAATGAGCCACAGAGAGTGAAGAGCCCTTTCAAGGGCGCCTGCAGTGAAT	660
Db	601	GAGTATCGGAATGGCCACAGAGAGTGAAGAGCCCTTTCAAGGGCGCCTGCAGTGAAT	660
Qy	661	GGCAGCAAGGACCTTGCAGAGACGTGTCCATCACTGTGCTCAACGTCACTTGAACGACTCT	720
Db	661	GGCAGCAAGGACCTTGCAGAGACGTGTCCATCACTGTGCTCAACGTCACTTGAACGACTCT	720
Qy	721	GGCCCTTACACCTGCAATGTGTCCCGGGAAGTTGAGTTGAGGGGCAATCGAGCCCTTTGTG	780
Db	721	GGCCCTTACACCTTCAATGTGTCCCGGGAAGTTGAGTTGAGGGGCAATCGAGCCCTTTGTG	780
Qy	781	AAGACGACGCGCGCTGATCCCTTAAGATGACCCGAGAGGCGTGAAGAGACTTCACTCT	840
Db	781	AAGACGACGCGCGCTGATCCCTTAAGATGACCTGAAGAGGCGTGAAGAGACTTCACTCT	840
Qy	841	GTGGTCTCAGAAATCATGATGTATATCTCTTGTGTCTTCTCAACCTGTGTGCTGTATC	900
Db	841	GTGGTCTCAGAAATCATGATGTATATCTCTTGTGTCTTCTCAACCTGTGTGCTGTATC	900
Qy	901	GAGATGATATATTGTCTACAGAAAGTCTCAAAAGCCGAAAGGCGACGCCCAAGAAACGCG	960
Db	901	GAGATGATATATTGTCTACAGAAAGTCTCAAAAGCCGAAAGGCGACGCCCAAGAAACGCG	960
Qy	961	TCTGACTACCTTGGCCATCCCATCTTGAGACAAGAGAACTCTGTGGGTATCCATGTGAGGAA	1020
Db	961	TCTGACTACCTTGGCCATCCCATCTTGAGAAACAGAGAACTCTGTGGGTATCCATGTGAGGAA	1020
Qy	1021	TAGAACAGGAGCAGTGTGACATGTAGGTGGCCCTGAACACTGAGGGGACTGGACATCCCATG	1080
Db	1021	TAGAACAGGAGCAGTGTGACATGTAGGTGGCCCTGAACACTGAGGGGACTGGACATCCCATG	1080
Qy	1081	TTGACCAATGTCAATGGCATCAGAGAGGGCGCCCAAGGGGCCCATTCGCTTCCCTTCATGC	1140
Db	1081	TTGACCAATGTCAATGGCATCAGAGAGGGCGCCCAAGGGGCCCATTCGCTTCCCTTCATGC	1140
Qy	1141	ATCCATTTGTTCTGTTCAATTCATTCATACATCCACCTGACCTGTGACCTTCACTCT	1200
Db	1141	ATCCATTTGTTCTGTTCAATTCATTCATACATCCACCTGACCTGTGACCTTCACTCT	1200
Qy	1201	GACTCCCTTAACCTCATGAGACCTTACGCAACATAAAGCTCTGCGAAGACTGAGAAACCG	1260
Db	1201	GACTCCCTTAACCTCATGAGACCTTACGCAACATAAAGCTCTGCGAAGACTGAGAAACCG	1260
Qy	1261	G 1261	
Db	1261	G 1261	
RESULT 4			
ABA93727			
ID	ABA93727	standard; cDNA; 4052 BP.	
XX	AC	ABA93727;	
XX	DT	30-APR-2002 (first entry)	
XX	DE	Human signal transduction cDNA clone amy2_2f18.	
XX	KM	Human; foetal brain; foetal kidney; melanoma; testis; amygdala;	
XX	KM	gene therapy; ss.	
XX	OS	Homo sapiens.	
XX	FN	WO200198454-A2.	
XX	PD	27-DEC-2001.	

XX 25-APR-2001; 2001MO-IB002050.  
 XX 25-APR-2000; 2000US-0199380P.  
 PR (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 PA Wiemann S;  
 PI WPI; 2002-055860/07.  
 DR P-PSDB; ABB05689.  
 XX Human cDNA sequences and clones derived from human fetal brain, fetal  
 PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic  
 PT screening and therapy.  
 XX Claim 1; Page 174-175; 611pp; English.  
 PS  
 XX The present invention describes assemblies and computer readable media  
 CC comprising novel human cDNA sequences and clones derived from human  
 CC fetal brain, foetal kidney, melanoma, testis and amygdala cDNA  
 CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the  
 CC present invention which encode the proteins given in ABB05662 to  
 CC ABB05729. The human cDNA sequences and clones can be used in gene  
 CC therapy. The clones may be used in a variety of applications, for example  
 CC they may be used in profiling assays, for providing large arrays of human  
 CC genetic material for implementing large-scale screening strategies and  
 CC for treating diseases via gene therapy procedures  
 CC  
 XX Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;  
 SQ  
 Query Match: 99.3%; Score 1252.2; DB 6; Length 4052;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 971 CACCACGGTGTGAATGTTCTACAGAGCCCGAGGCGGTAAAGATTCTTATTACGA 1030  
 Qy 603 GTATCGGAATGGCCACACAGAGAGTGGAGAGCCCTTACAGGGCGCTGAGTGAATGG 662  
 Db 1031 GTATCGGAATGGCCACACAGAGAGTGGAGAGCCCTTACAGGGCGCTGAGTGAATGG 1090  
 Qy 663 CACCAAGAGACCTGACAGAGCGTGTCCATCACTGTGCTCAACGTCACCTGTAACACTGTGG 722  
 Db 1091 CACCAAGAGACCTGACAGAGCGTGTCCATCACTGTGCTCAACGTCACCTGTAACACTGTGG 1150  
 Qy 723 CCTCTACCTGCAATGTGTCCCGGAGATTGAGTTGAGGCGCATCGCCCTTTGTGAA 782  
 Db 1151 CCTCTACCTGCAATGTGTCCCGGAGATTGAGTTGAGGCGCATCGCCCTTTGTGAA 1210  
 Qy 783 GACGAGCGGCTGATCCCTTAAGAGTACCCGAGAGGCTGAGAGAGACTTCACTCTGT 842  
 Db 1211 GACGAGCGGCTGATCCCTTAAGAGTACCCGAGAGGCTGAGAGAGACTTCACTCTGT 1270  
 Qy 843 GGTCTGAAATCATGATGATCATCTTCTGTGCTTCTTCCACCTGTGGCTCATCGA 902  
 Db 1271 GGTCTGAAATCATGATGATGATCATCTTCTGTGCTTCTTCCACCTGTGGCTCATCGA 1330  
 Qy 903 GATGATATATTTGCTACAGAAAGGTTCAAAAGCCGAGAGAGAGAGAGAGAGAGAGAG 962  
 Db 1331 GATGATATATTTGCTACAGAAAGGTTCAAAAGCCGAGAGAGAGAGAGAGAGAGAGAG 1390  
 Qy 963 TGACTACCTTGTGCTATCCCATCTGAGAACAAAGAGAACTCTGCGGTACAGTGAAGATA 1022  
 Db 1391 TGACTACCTTGTGCTATCCCATCTGAGAACAAAGAGAACTCTGCGGTACAGTGAAGATA 1450  
 Qy 1023 GAACAGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1082  
 Db 1451 GAACAGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1510  
 Qy 1083 CAGCAATGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1142  
 Db 1511 CAGCAATGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1570  
 Qy 1143 CCAATTGTTCTGTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1202  
 Db 1571 CCAATTGTTCTGTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1630  
 Qy 1203 CTCCTTAATCCATCAGACCTCTAGACACCATTAAGACTCTGCGAGAACTGAGAAGCC 1259  
 Db 1631 CTCCTTAATCCATCAGACCTCTAGACACCATTAAGACTCTGCGAGAACTGAGAAGCC 1687

RESULT 5  
 AAF84146  
 ID AAF84146 standard; cDNA; 1510 BP.  
 AC AAF84146;  
 XX  
 XX 07-SEP-2001 (first entry)  
 XX  
 DE Human novel sodium channel beta1-like subunit encoding cDNA.  
 XX  
 XX Sodium channel; sensory neurone specific channel; beta1-like subunit;  
 KW SNS; therapeutic; pain; analgesic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 213..860  
 FT /\*tag= a  
 FT /product= "sodium channel beta1-like subunit"  
 XX  
 PN MO200144293-A2.  
 XX  
 XX 21-JUN-2001.  
 XX  
 XX 14-DEC-2000; 2000MO-GB004802.  
 XX

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PR 17-DEC-1999; 99GB-00029970.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Plimpton M, Powell AJ, Sanseau P;
XX
XX WPI; 2001-398129/42.
XX
XX P-PSDB; AAB85206.
XX
XX Novel sub-unit for voltage-gated sodium channel proteins for producing
XX agents useful for treating pain.
XX
XX Claim 4; Page 29-30; 31pp; English.
XX
XX The invention provides a novel beta1-like sub-unit for voltage-gated
XX sodium ion channel polypeptide, specifically a sensory neuron specific
XX channel (SNS) subunit. The novel beta1-like subunit is useful for
XX producing a therapeutic agent which is useful treating pain in a patient.
XX The subunit can be expressed by standard recombinant methodology. The
XX present sequence represents a human novel sodium channel beta1-like
XX subunit encoding cDNA
XX
XX Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other;
XX
XX Query Match 72.1%; Score 909.4; DB 4; Length 1510;
XX Best Local Similarity 99.9%; Pred. No. 3.4e-234;
XX Matches 910; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 349 AGCCTTGGAAAGCCGACGAGCCCAAGAAATGCTGCTTCAATAGATTGTTTCCCTGCT 408
DB 186 AGCCTTGGAAAGCCGACGAGCCCAAGAAATGCTGCTTCAATAGATTGTTTCCCTGCT 245
QY 409 TCTCTGCTTATCTACTAGTGGTCACTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCT 468
DB 246 TCTCTGCTTATCTACTAGTGGTCACTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCT 305
QY 469 GAGAGGAGGCGCGTGCAGGAGCAACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
DB 306 GAGAGGAGGCGCGTGCAGGAGCAACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
QY 529 GAGAGGAGGCGCGTGCAGGAGCAACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
DB 366 GAGAGGAGGCGCGTGCAGGAGCAACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
QY 589 TTCCTTATTTAGAGTATGGAATGAGGAGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 648
DB 426 TTCCTTATTTAGAGTATGGAATGAGGAGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 485
QY 649 CTGCAAGTGAATGAGGAGCAAGGAGCTGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
DB 486 CTGCAAGTGAATGAGGAGCAAGGAGCTGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
QY 709 CTGAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
DB 546 CTGAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
QY 769 CGGCGCTTTGTAAGCAAGCGGCGTGAATCCCTTAAGAGTACACGAGGAGGCTGAGAG 828
DB 606 CGGCGCTTTGTAAGCAAGCGGCGTGAATCCCTTAAGAGTACACGAGGAGGCTGAGAG 665
QY 829 GACTTCACTCTGTGTGCTCAGAAATCATGATGATCATCTTCTGCTTCTTCTCAACCTG 888
DB 666 GACTTCACTCTGTGTGCTCAGAAATCATGATGATCATCTTCTGCTTCTTCTCAACCTG 725
QY 889 TGGCTGCTCATGAGATGATATATTTGCTACAGAAAGGTCTCAAAAGCCGAGAGGAGGAGCC 948
DB 726 TGGCTGCTCATGAGATGATATATTTGCTACAGAAAGGTCTCAAAAGCCGAGAGGAGGAGCC 785
QY 949 CAAGAAAGCGGCTGAGTACCTTGCAATCCGATCGAGAAACAAGAGAACTCTGCGGTA 1008
DB 786 CAAGAAAGCGGCTGAGTACCTTGCAATCCGATCGAGAAACAAGAGAACTCTGCGGTA 845
QY 1009 CCAATGAGGAATAGAAACAGAGAGAGTGTGACATGAGGTGCGCTGAAACACTGAGGAGACT 1068
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DB 846 CCAGTGGAGGAATAGAACAGAGAGAGTGTGACATGAGGTGCTGAAACCTTGAGGAGACT 905
QY 1069 GAGATCCCGATGTTGAGCAATGATCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1128
DB 906 GAGATCCCGATGTTGAGCAATGATCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 965
QY 1129 TTCCCTTCATGATCATGATGTTGCTGCTTCAATTCATTCATTCATTCATTCATTCATTCAT 1188
DB 966 TTCCCTTCATGATCATGATGTTGCTGCTTCAATTCATTCATTCATTCATTCATTCATTCAT 1025
QY 1189 GCTTTCACCTCTGACTCCCTTAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1248
DB 1026 GCTTTCACCTCTGACTCCCTTAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1085
QY 1249 ACTGAGAGGCC 1259
DB 1086 ACTGAGAGGCC 1096
XX
XX RESULT 6
XX AAK52345
XX ID AAK52345 standard; cDNA; 1045 BP.
XX
XX AAK52345;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 890.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX
XX (HISE-) HISEQ INC.
XX
XX Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX P-PSDB; AAM79212.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 1; Page 2934-2935; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, hematopoiesis regulating
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OY 326 TGACCGAGGAATCTCTGTGTAGCTTGAAAGCCGACGCCAGAAAGATGCTGCT 385
XX
DB 245 TGACCGAGGAATCTCTGTGTAGCTTGAAAGCCGACGCCAGAAAGATGCTGCT 304
OY 386 TCAATAGATTTTCCCTGCTTCTGTGTGCTTATCTACGTGGTCAATGCTGCTTC 445
DB 305 TCAATAGATTTTCCCTGCTTCTGTGTGCTTATCTACGTGGTCAATGCTGCTTC 364
OY 446 CTGTGTGTGGAAGTGCCTCGAGACGAGAGCCGTGAGGGCAACCCCATGAAGCTGC 505
DB 365 CTGTGTGTGGAAGTGCCTCGAGACGAGAGCCGTGAGGGCAACCCCATGAAGCTGC 424
OY 506 GCTGCATCTCTGCATGAAGAGAGAGAGTGAAGCCACACGCTGTGAATGCTTC 565
DB 425 GCTGCATCTCTGCATGAAGAGAGAGAGTGAAGCCACACGCTGTGAATGCTTC 484
OY 566 AAGAGCCGAGAGGCGGTAAAGATTTCTTATTATGAGATATGGATGGCCACGAGAG 625
DB 485 AAGAGCCGAGAGGCGGTAAAGATTTCTTATTATGAGATATGGATGGCCACGAGAG 544
OY 626 TGAAGAGCCCTTTCAAGGGGCGCTGCACTGGAATGGACGAAGACCTGACGAGCTGT 685
DB 545 TGAAGAGCCCTTTCAAGGGGCGCTGCACTGGAATGGACGAAGACCTGACGAGCTGT 604
OY 686 CCATCACTGTGCTCAACGTCACCTGGAACGACTTGGCTTACACCTGCAATGTGCTCC 745
DB 605 CCATCACTGTGCTCAACGTCACCTGGAACGACTTGGCTTACACCTGCAATGTGCTCC 664
OY 746 GGAATTTGAGTTTGAAGGCGCATCGGCTTTGTGAAGACGAGCGGGCTGATCCCCCTTA 805
DB 665 GGAATTTGAGTTTGAAGGCGCATCGGCTTTGTGAAGACGAGCGGGCTGATCCCCCTTA 724
OY 806 GAGTCAACGAGAGGCTGGAAGAGACTTCACTGTGTGCTCAAGAAATCATGATGTACA 865
DB 725 GAGTCAACGAGAGGCTGGAAGAGACTTCACTGTGTGCTCAAGAAATCATGATGTACA 784
OY 866 TCTTTCTGTGCTCTTCAACCTGTGTGCTGCTCATGAGATGATATATG-CTACAGAAAG 924
DB 785 TCTTTCTGTGCTCTTCAACCTGTGTGCTGCTCATGAGATGATATATG-CTACAGAAAG 844
OY 925 GCTTCAAAAGCCGAGAGGCAAGCCCAAGAAACGCTGTGATACCT-TTGCCATCCCATC 983
DB 845 GCTTCAAAAGCCGAGAGGCAAGCCCAAGAAACGCTGTGATACCT-TTGCCATCCCATC 904
OY 984 TGAGAAACAAGAGAACTGCGGTACCAAGTGAAGAA 1020
DB 905 TGAGAAACAAGAGAAATTTCTTCGTACCTGCGGGGGA 941
```

RESULT 8  
ADS11487  
ID ADS11487 standard; DNA; 978 BP.

XX ADS11487;

XX 16-DEC-2004 (first entry)

DE Human therapeutic contig DNA - SEQ ID 1724.

XX antiinflammatory; neuroprotective; antianaemic; cyrostatic; vulnerary;  
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
XX aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

OS Homo sapiens.

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX

PA (NUVE-) NUVELO INC.  
XX  
PI Tang YF, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
XX WPI; 2004-668857/65.  
DR P-PSDB; ADS12085.  
XX  
XX New polynucleotide, useful in preparing a composition for diagnosing or  
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
PT aplastic anemia or cancer for promoting wound healing.  
XX

PS Example 2; SEQ ID NO 1724; 718bp; English.

XX  
XX The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianaemic, cyrostatic and vulnerary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC disorders, such as aplastic anaemia or cancer, as well as for promoting  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic contig  
CC DNA of the invention. The current sequence is not shown explicitly within  
CC the specification but can be accessed from the WIPO web-site.  
XX

Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Query Match 68.1%; Score 858.6; DB 13; Length 978;

Best Local Similarity 96.2%; Pred. No. 1.4e-220; Mismatches 34; Indels 2; Gaps 2;

Matches 901; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

OY 86 GAGCGCATGTCCTGCTGTGCTGAGCGCGGAGAGCGGAGCGGCTGATCGACT 145

DB 5 GTGGGCACTGTGCTGCTGCTGAGCGCGGAGAGCGGAGCGGCTGATCGACT 64

OY 146 CCTTGAACTGAGAGGTTCAGTGGGGTGTGCTTGAAGCCCAAGCCCATCCGGCTCA 205

DB 65 CCTTGAACTGAGAGGTTCAGTGGGGTGTGCTTGAAGCCCAAGCCCATCCGGCTCA 124

OY 206 AAAGTCCCAAGGCGCTCCCAAGGACCGGAGCTGGGCTCTTGGTCAAGAAAGTGC 265

DB 125 AAAGTCCCAAGGCGCTCCCAAGGACCGGAGCTGGGCTCTTGGTCAAGAAAGTGC 184

OY 266 CCCCTGGGGGAGTTCGTCGCAAAAGGTTCTCGAAAGAACTGAGAGGCGGAGTCT 325

DB 185 CCCCTGGGGGAGTTCGTCGCAAAAGGTTCTCGAAAGAACTGAGAGGCGGAGTCT 244

OY 326 TGACCGAGGAAATCTCTGTGTAGCTTGAAGCGCCGACGCCCAAGAAATGCTGCT 385

DB 245 TGACCGAGGAAATCTCTGTGTAGCTTGAAGCGCCGACGCCCAAGAAATGCTGCT 304

OY 386 TCAATAGATTTTCCCTGGGCTTCTCGGCTTATCTACGGGTGAGTGTGCTTCC 445

DB 305 TCAATAGATTTTCCCTGGGCTTCTCGGCTTATCTACGGGTGAGTGTGCTTCC 364

OY 446 CTGTGTGTGGAAGTGCCTCGAGACGAGGCGGTGACAGGCAACCCCATGAAGCTGC 505

DB 365 CTGTGTGTGGAAGTGCCTCGAGACGAGGCGGTGACAGGCAACCCCATGAAGCTGC 424

OY 506 GCTGCATCTCTGCATGAAGAGAGAGTGAAGGCCACACGCTGTGAATGCTTCT 565

DB 425 GCTGCATCTCTGCATGAAGAGAGAGTGAAGGCCACACGCTGTGAATGCTTCT 484

OY 566 AAGGCGCGAGAGGCGGTAAAGATTTCTTATTATGAGATATGGAATGGCCACAGAGG 625

DB 485 AAGGCGCGAGAGGCGGTAAAGATTTCTTATTATGAGATATGGAATGGCCACAGAGG 544

OY 626 TGAAGAGCCCTTTCAAGGGGCGCTGACAGTGAATGAGAGAACTGACGAGACGTGT 685

DB 545 TGAAGAGCCCTTTCAAGGGGCGCTGACAGTGAATGAGAGAACTGACGAGACGTGT 604

OY 686 CCATCACTGTGCTCAACGTCATGAAGACGCTTGGCTTACACCTGCAATGTGCTCC 745

Db	605	CCATCAGCTGTGCTCAACGTCACCTGTGAAGACTCTGACCTCTACACCTGCATGTGTGCC	664
Qy	746	GGGACATTTGACGTTTGAAGGGCATTCGGCCCTTTGTGAAGACGACGGCTGATCCCCCTAA	805
Db	665	GGGACATTTGAGTTTGAAGGGGACATCGGCCCTTTGTGAAGACGACGGCTGATCCCCCTAA	724
Qy	806	GAGTCACGAGAGAGGCTGAGAGGAACTTCAACCTCTGTGATCTGAGAAATCATGATGTACA	865
Db	725	GAGTCACGAGAGAGGCTGAGAGGAACTTCAACCTCTGTGATCTGAGAAATCATGATGTACA	784
Qy	866	TCCCTTCTGGTCTTCTCTCAACCTGTGGCTGCTCATCGAGATGATATATTTG-CTACAGAAAG	924
Db	785	TCCCTTCTGGTCTTCTCTCAACCTGTGGCTGCTCATCGAGATGATATATTTGCTACAGAACG	844
Qy	925	GTCCTAAAAGCCGAGAGGACGCCCAAGAAAACGGCTTGACATACC-TTGCCATCCCATC	983
Db	845	GTGATCAACAGAGAAACGAGCCGCCCAAGAAAACCGAATGGCTACCTTTGGCGATTCATT	904
Qy	984	TGAGAACAGAGAACTCTGCGGTACCACTGAGAGAA	1020
Db	905	TGAGAACAGAGAAATTTCTCGGTACTCTCGGGGGGA	941
RESULT 9			
ADSL0151	ID	ADSL0151 standard; DNA; 953 BP.	
XX	ADSL0151;		
XX	16-DEC-2004	(first entry)	
XX	DE	Human therapeutic DNA - SEQ ID 388.	
XX	DE	antiinflammatory; neuroprotective; antianaemic; cyostatic; vulnerax;	
KW	KW	inflammatory; haematopoesis; immunity; neurodegenerative; stem cell;	
KW	KW	aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	WO2004080148-A2.	
PD	PD	23-SEP-2004.	
XX	XX		
PF	PF	30-SEP-2003; 2003WO-US030720.	
XX	XX		
PR	PR	02-OCT-2002; 2002US-0416186P.	
XX	XX		
PA	PA	(NIVE-) NIVELO INC.	
XX	XX		
PI	PI	Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y,	
PI	PI	Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P,	
XX	XX	WPI; 2004-668857/65.	
DR	DR	P-PSDB; ADSI0835.	
PT	PT		
PT	PT	New polynucleotide, useful in preparing a composition for diagnosing or	
PT	PT	treating inflammatory, neurodegenerative or stem cell disorders, e.g.,	
XX	XX	aplastic anemia or cancer for promoting wound healing.	
PS	PS	Claim 1; SEQ ID NO 388; 718bp; English.	
XX	XX		
CC	CC	The invention relates to a novel isolated polynucleotide and the encoded	
CC	CC	polypeptide. The molecules of the invention demonstrate antiinflammatory,	
CC	CC	neuroprotective, antianaemic, cyostatic and vulnerary activities and may	
CC	CC	be useful in preparing a composition for diagnosing or treating	
CC	CC	inflammatory, haematopoietic, immune, neurodegenerative or stem cell	
CC	CC	disorders, such as aplastic anaemia or cancer, as well as for promoting	
CC	CC	wound healing. The molecules may also be utilised during gene therapy	
CC	CC	procedures. The current sequence is that of a human therapeutic DNA of	
CC	CC	the invention. The current sequence is not shown explicitly within the	
XX	XX	specification but can be accessed from the WIPO web-site.	
QO	QO	Sequence 953 BP; 180 A; 279 C; 290 G; 204 T; 0 U; 0 Other;	

Query Match	62.8%;	Score 792.4;	DB 13;	Length 953;
Best Local Similarity	99.3%;	Pred. No. 9e-203;		
Matches	796;	Conservative	0;	Mismatches 6; Indels 0; Gaps 0;
QY	86	GAGCGACGTGCTCCGTGTGTCTGACGCGCGGCGAGAGCGGGCGCGAGCGGCTGATCGACT	145	
DB	37	GTGGCGACTGTCCGTGTGTGTGACGCGCGGCGAGAGCGGGCGCGAGCGGCTGATCGGCT	96	
QY	146	CCCTCGAAGCTGGGGAGGTCAGGTGGGGTGTGCTTAAGGGCCCAAGCCCCACCCGGGCTTCA	205	
DB	97	CCCTCGAAGCTGGGGAGGTCAGGTGGGGTGTGCTTAAGGGCCCAAGCCCCACCCGGGCTTCA	156	
QY	206	AAAGCTCCCAAGGGGCTCCCGCAGGACCGGAGCTCGGCGCTTCTCTCGGTAGAAGTGGC	265	
DB	157	AAAGCTCCCAAGGGGCTCCCGCAGGACCGGAGTCTCGGCGCTTCTCTCGGTAGAAGTGGC	216	
QY	266	CCCTCGGGGGCAGTTGCTCCCAAGGGTTTCTCTGAAAGAACTGAGAGGGCGCAGTCT	325	
DB	217	CCCTCGGGGGCAGTTGCTCCCAAGGGTTTCTCTGAAAGAACTGAGAGGGCGCAGTCT	276	
QY	326	TGACCGAGGGAAATCTCTGTGTAGCCTTGGAGGCGGCGCCGCAAGATGTCTGCT	385	
DB	277	TGACCGAGGGAAATCTCTGTGTAGCCTTGGAGGCGGCGCCGCAAGATGTCTGCT	336	
QY	386	TCAATAAGATTGTTCCCTGGCTTCTCTCGGCTTATCTACTGGGTGAGTGTCTGCTTC	445	
DB	337	TCAATAAGATTGTTCCCTGGCTTCTCTCGGCTTATCTACTGGGTGAGTGTCTGCTTC	396	
QY	446	CTGTGTGTGTGAAGTGCCTTCGAGACGGAAGCGCGTGCAGAGGCAACCCCATGAAGTGC	505	
DB	397	CTGTGTGTGTGAAGTGCCTTCGAGACGGAAGCGCGTGCAGAGGCAACCCCATGAAGTGC	456	
QY	506	GCTGCATCTCTGTGATGAAGAGAGAGAGTGAAGGCACACGCTGTGGAAATGTCT	565	
DB	457	GCTGCATCTCTGTGATGAAGAGAGAGTGAAGGCACACGCTGTGGAAATGTCT	516	
QY	566	ACAGGCCCGAGGGCGGTAAAGATTCTTATTTAAGAGTATCGGAATGAGCCACGAGAG	625	
DB	517	ACAGGCCCGAGGGCGGTAAAGATTCTTATTTAAGAGTATCGGAATGAGCCACGAGAG	576	
QY	626	TGAGAGCCCTTTCAGGGGCGCTCGAGTGAATGGACGACGACCTTCGAGAGCTGT	685	
DB	577	TGAGAGCCCTTTCAGGGGCGCTCGAGTGAATGGACGACGACCTTCGAGAGCTGT	636	
QY	686	CGATCACTGTGTCAAGTCACTCACTTGAAGCACTCTGGCCCTTACACTTGGAAATGTCTCC	745	
DB	637	CGATCACTGTGTCAAGTCACTTGAAGCACTCTGGCCCTTACACTTGGAAATGTCTCC	696	
QY	746	GGAGATTGAGTTGAGGGCGCATCGGCCCTTGTGAAAGACGAGCGGCTATCCCCCTAA	805	
DB	697	GGAGATTGAGTTGAGGGCGCATCGGCCCTTGTGAAAGACGAGCGGCTATCCCCCTAA	756	
QY	806	GAGTCACTCGAGAGAGCTGAGAGAGACTTCACTCTGTGTCTCAGAAATCATGATGTACA	865	
DB	757	GAGTCACTCGAGAGAGCTGAGAGAGACTTCACTCTGTGTGTCTCAGAAATCATGATGTACA	816	
QY	866	TTCCTTGTGTCTTCTTCACCCCT	887	
DB	817	TTCCTTGTGTGTCTTCTTCACCCCT	838	
RESULT 10				
AAS86764				
ID	AAS86764 standard; cDNA; 1195 BP.			
XX	AAS86764;			
XX	13-FEB-2002 (first entry)			
XX	DNA encoding novel human diagnostic protein #22568.			
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;			



KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI, 2001-639362/73.  
XX P-PSDB; ABG22577.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostic, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity.  
XX  
XX Claim 1; SEQ ID NO 22568; 103bp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotide are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 1195 BP; 253 A; 356 C; 381 G; 205 T; 0 U; 0 Other;

Query Match 44.6%; Score 561.8; DB 5; Length 1195;  
Best Local Similarity 95.8%; Pred. No. 1.2e-140;  
Matches 599; Conservative 0; Mismatches 22; Indels 4; Gaps 2;

349 AGCCTTGAAAGCCGCGAGCCCGAAGATCGCTTCATATGATTTGTCCTCGGCT 408  
436 AGCCTTGAAAGCCGCGAGCCCGAAGATCGCTTCATATGATTTGTCCTCGGCT 495  
409 TCTCTGCTCTTATCTACTGAGTGTGCTGCTTCCCTGTGTGTGAA--GTGCCCT 466  
496 TCTCTGCTCTTATCTACTGAGTGTGCTGCTTCCCTGTGTGTGAAAGTGCCTT 555  
467 CGGAGACGGAGGCGCGTGA--GGGCAACCCCAATGAAGTGGGCTGCATCCCGATGAA 524  
556 AAAAAACGGGGGCGGCGACGCGCTTAACCCCAATGAAGTGGGCTGCATCCCGATGAA 615  
525 GAGAGAGAGGTGAGAGCCACCAAGTGTGTGAATGTTCTACAGGCCCGAGGCGGTAA 584  
616 GAGAGAGAGGTGAGAGCCACCAAGTGTGTGAATGTTCTACAGGCCCGAGGCGGTAA 675  
585 AGATTTCCTTATTTACGATATCGAATGGCCACAGAGGTGAGAGGCCCTTTCAAGG 644  
|||||

DB 676 AGATTTCCTTATTTACGATATCGAATGGCCACAGAGAGGTGAGAGGCCCTTTCAAGG 735  
QY 645 GCGCCTGAGTGAATGGCAGCAAGACCTTGACAGACGTGTCCATCACTGTGCTCAAGCT 704  
DB 736 GCGCCTGAGTGAATGGCAGCAAGACCTTGACAGACGTGTGCTCAAGCT 795  
QY 705 CACTGTGAAGACCTGTGGCCTTCACTGCGCAATGTGTCCGGGAGTTGAGTTGAGGC 764  
DB 796 CACTGTGAAGACCTGTGGCCTTCACTGCGCAATGTGTCCGGGAGTTGAGTTGAGGC 855  
QY 765 GCATCGGCCCTTTGGAAGACGACGCGGCTGATCCCTTAAGATCAACGAGAGGCTGG 824  
DB 856 GCATCGGCCCTTTGGAAGACGACGCGGCTGATCCCTTAAGATCAACGAGAGGCTGG 915  
QY 825 AGAGACTTCACTCTGTGTGTCTAGAAATCATGATGATCATCTTGTGTCTTCTCAC 884  
DB 916 AGAGACTTCACTCTGTGTGTCTAGAAATCATGATGATGATCATCTTGTGTCTTCTCAC 975  
QY 885 CCTGTGGCTGCTCATCGAGATGATATTTGCTACAGAAAGGTTCCAAAGCCGAAGAGGC 944  
DB 976 CTTGTGGCTGCTCATCGAGATGATATTTGCTACAGACAGGTTCTCAAAAGCCGAAGAGGC 1035  
QY 945 AGCCCAAGAAAACGGGTCTGACTAC 969  
DB 1036 AGCCCAAGAAAACGGGTCTGACTAC 1060

RESULT 11

AAC90602  
ID AAC90602 standard; DNA; 2632 BP.

AC AAC90602;

DT 13-MAR-2001 (first entry)

DE Rat sodium channel beta3 protein Alrx94h5 related sequence.

XX Rat; sodium channel beta3 protein; Alrx94h5; pair; sleep disorder;

KW neurodegenerative disorder; mood disorder; muscle contraction; ds.

XX Rattus sp.

XX WO200069912-A1.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US013144.

XX 14-MAY-1999; 99US-0134198P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ;

XX WPI, 2001-122743/13.

XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal

PT root ganglion cDNA library for use in chromosome mapping, forensic

PS medicine, monitoring clinical trials and therapeutics.

XX Claim 1; Page 41-42; 145bp; English.

The present invention provides the protein and coding sequences of the rat sodium channel beta3 protein, designated Alrx94h5. This protein is involved in the generation of pain and other sensory or perceptible nerve impulses, in the establishment and endurance of mood, neurodegenerative and sleep disorders, and in the control of muscle contraction, including movements such as the heartbeat, digestion and vascular tone. The CC sequences can be used in predictive medicine, screening and diagnostic assays, and in pharmacogenomics

XX Sequence 2632 BP; 693 A; 636 C; 611 G; 692 T; 0 U; 0 Other;



Query Match 44.4%; Score 559.6; DB 5; Length 2632;  
 Best Local Similarity 84.4%; Pred. No. 6.5e-140;  
 Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

QY 371 AGAAGATGCTGCTTCAATAGATTGTTTCCCTGCTTCTCTGCTTATCTACTGGG 430  
 DB 73 AAAAGATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTGCTATCTACTGGG 132  
 QY 431 TCAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490  
 DB 133 TCAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192  
 QY 491 ACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550  
 DB 193 ATCCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 252  
 QY 551 TGTGTGAATGCTTCTACAGGCGCGAGGCGGTAAAGATTTCTTATTTACGATATGGA 610  
 DB 253 TGTGTGAATGCTTCTACAGGCGCGAGGCGGTAAAGATTTCTTATTTACGATATGGA 312  
 QY 611 ATGGCCACCGAGAGTGAAGAGCCCTTTCAAGGGCGCTGCTGCTGCTGCTGCTGCTG 670  
 DB 313 ATGGCCACCGAGAGTGAAGAGCCCTTTCAAGGGCGCTGCTGCTGCTGCTGCTGCTG 372  
 QY 671 ACCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730  
 DB 373 ACCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432  
 QY 731 CTTGCAATGTGTCCCGGAGTTTGAAGGCGCATCGGCTTTTGTGAAGAGAGCGC 790  
 DB 433 CATGCAATGTGTCCCGGAGTTTGAAGGCGCATCGGCTTTTGTGAAGAGAGCGC 492  
 QY 791 GGCTGATCCCTTCAAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850  
 DB 493 GAGTGAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552  
 QY 851 AAATCATGATGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 910  
 DB 553 AAATCATGATGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612  
 QY 911 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970  
 DB 613 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672  
 QY 971 TTGCGCATCCCATCTGAG 1030  
 DB 673 TTGCGCATCCCATCTGAG 726  
 QY 1031 GCAGTGTGATGATGAG 1090  
 DB 727 GTGCTGTGATGATGAG 785  
 QY 1091 TCATGAGCATCAG 1146  
 DB 786 CAGAGCATATCAG 841

RESULT 12  
 AAC90600  
 ID AAC90600 standard; cDNA; 3108 BP.  
 AC AAC90600;  
 XX  
 DT 13-MAR-2001 (first entry)  
 DE  
 XX Rat sodium channel beta3 protein Alrx94h5 coding sequence.  
 XX  
 KM Rat; sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;  
 XX neurodegenerative disorder; mood disorder; muscle contraction; ss.  
 OS Rattus sp.  
 XX  
 PN MO200069912-Al.

XX  
 PD 23-NOV-2000.  
 XX  
 PF 12-MAY-2000; 2000MO-US0113144.  
 XX  
 PR 14-MAY-1999; 99US-0134198P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PT Curtis RAD;  
 XX  
 DR WPI; 2001-122743/13.  
 XX  
 DR P-PSDB; AAB50243, AAB50245.  
 PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal  
 PT root ganglion cDNA library for use in chromosome mapping, forensic  
 PT medicine, monitoring clinical trials and therapeutics.  
 XX  
 PS Claim 1; Fig 1; 145pp; English.

CC The present invention provides the protein and coding sequences of the  
 CC rat sodium channel beta3 protein, designated Alrx94h5. This protein is  
 CC involved in the generation of pain and other sensory or perceptive nerve  
 CC impulses, in the establishment and endurance of mood, neurodegenerative  
 CC and sleep disorders, and in the control of muscle contraction, including  
 CC movements such as the heartbeat, digestion and vascular tone. The  
 CC sequences can be used in predictive medicine, screening and diagnostic  
 CC assays, and in pharmacogenomics

XX  
 SQ Sequence 3108 BP; 830 A; 748 C; 727 G; 803 T; 0 U; 0 Other;

Query Match 44.4%; Score 559.6; DB 5; Length 3108;  
 Best Local Similarity 84.4%; Pred. No. 7e-140;  
 Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

QY 371 AGAAGATGCTGCTTCAATAGATTGTTTCCCTGCTTCTCTGCTTATCTACTGGG 430  
 DB 73 AAAAGATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTGCTATCTACTGGG 132  
 QY 431 TCAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490  
 DB 133 TCAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192  
 QY 491 ACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550  
 DB 193 ATCCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 252  
 QY 551 TGTGTGAATGCTTCTACAGGCGCGAGGCGGTAAAGATTTCTTATTTACGATATGGA 610  
 DB 253 TGTGTGAATGCTTCTACAGGCGCGAGGCGGTAAAGATTTCTTATTTACGATATGGA 312  
 QY 611 ATGGCCACCGAGAGTGAAGAGCCCTTTCAAGGGCGCTGCTGCTGCTGCTGCTGCTG 670  
 DB 313 ATGGCCACCGAGAGTGAAGAGCCCTTTCAAGGGCGCTGCTGCTGCTGCTGCTGCTG 372  
 QY 671 ACCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730  
 DB 373 ACCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432  
 QY 731 CTTGCAATGTGTCCCGGAGTTTGAAGGCGCATCGGCTTTTGTGAAGAGAGCGC 790  
 DB 433 CATGCAATGTGTCCCGGAGTTTGAAGGCGCATCGGCTTTTGTGAAGAGAGCGC 492  
 QY 791 GGCTGATCCCTTCAAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850  
 DB 493 GAGTGAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552  
 QY 851 AAATCATGATGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 910  
 DB 553 AAATCATGATGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612  
 QY 911 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970

DB 613 ATTGCTACAGAAAGTCTTAAAGCCGAGAGGACAGACAGAAAATGCTGTGATACC 672  
QY 971 TTGCCATCCCATCTGTGAGAACAGAGAACTCTGCGGTACAGTGAGAGAAAGAGCA 1030  
DB 673 TTGCTATCCCTTCAGAGAACAGAGAACTCTGTGTACTGTGAGAGAAAT-AT 726  
QY 1031 GAGTGTGACATGAGGTGCGCTGAACACCTGAGAGGACTGGAATCCATGTTTCAAGATG 1090  
DB 727 GTGGTGTGACTTGAGGTGATCTG-AGTGTGAGAGGACTGGATATATCCCACTTCAAGTATG 785  
QY 1091 TCAATGACATCAGAGAGGCGCCCAAGAGGCCCTGCTGCTTCCCTTATCATTCAT 1146  
DB 786 CCAGCAATATCAGAGAGTGCCTCCAGGTGTCCCAACATCCATCTTTCTATTTCAT 841

RESULT 13  
AAC67836  
ID AAC67836 standard; cDNA; 2220 BP.  
AC AAC67836;  
XX  
XX 15-FEB-2001 (first entry)  
DE Rat beta3 subunit cDNA.  
XX  
XX Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;  
KM vasotrophic; cardiant; nootropic; cytostatic; dermatological;  
KM gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;  
KM ischaemia; heart disease; Jacobsen Syndrome;  
KM familial nonchromaffin paraganglioma; phenyleketonuria;  
KM Charcot Marie Tooth disease; ss.  
XX  
XX Rattus sp.  
OS  
XX WO20006367-A1.  
PN 26-OCT-2000.  
XX  
XX 24-FEB-2000; 2000WO-EP001783.  
PF  
XX 15-APR-1999; 99US-0129473P.  
PR  
XX (WARN) WARNER LAMBERT CO.  
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
PA  
XX Cox P, Dixon A, Jackson A, Morgan K;  
PI  
XX WPI; 2000-665241/64.  
DR P-PSDB; AAB36001.  
XX  
XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium  
PT channel, and their corresponding polypeptides, useful for detecting and  
PT treating sodium channel-associated conditions, e.g. pain, epilepsy and  
PT stroke.  
XX  
XX Claim 6; Page 69-70; 88pp; English.  
PS  
XX The present sequence is given in the claims of a specification relating  
CC to a novel family of beta sub-unit proteins from a voltage-gated sodium  
CC channel. Human and rat beta sub-units, which have been collectively  
CC identified as beta3, have been isolated. The polynucleotides and  
CC polypeptides are useful for screening for agonists and antagonists of  
CC sodium channels. The agonists, antagonists, proteins and nucleic acids  
CC may be used diagnosing of treating diseases or conditions associated with  
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,  
CC heart disease, Jacobsen Syndrome, familial Nonchromaffin Paraganglioma,  
CC Phenyleketonuria and Charcot Marie Tooth disease  
XX  
XX Sequence 2220 BP; 573 A; 557 C; 561 G; 529 T; 0 U; 0 Other;

Query Match 42.8%; Score 540; DB 3; Length 2220;  
Best Local Similarity 89.3%; Pred. No. 1.2e-134;  
Matches 582; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 371 AGAAGTCCCTGCTTCAATAGATTGTTTCCCTGCTTCTCTGCTTACTACTG 430  
DB 358 AAAAATGCTGCTTCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTACTACTG 417  
QY 431 TCAGTGTCTCTTCCCTGTGTGTGTGAAGTGCCTCGAGACGAGGCCCTGACAGGCA 490  
DB 418 TCAGAGTCTGCTTCCCTGTGTGTGTGAAGTGCCTCGAGACGAGGCCCTGACAGGCA 477  
QY 491 ACCCATAGAGTGTGCTGATCTCTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 550  
DB 478 ATCCATAGAGTGTGAGTCAATCTCTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537  
QY 551 TGTGGAATGTTTCTTCAAGAGCCCGAGGCGGTAAAGATTTCCTTATTAACAGATTCGGA 610  
DB 538 TGTGTGAGTGTGTTCTTCAAGAGCCGTAGAGGCGGTAAAGATTTCCTTATTAAGTATCGGA 597  
QY 611 ATGACCACAGAGAGGTGAGAGAGCCCTTTCAGAGGCGCTTCAAGTGTGAGATGACAGAGAG 670  
DB 598 ATGGCCACAGAGAGGTGAGAGAGCCCTTTCAGAGGCGCTTCAAGTGTGAGATGAGAGAGAG 657  
QY 671 ACCTGACAGAGAGTGTGATCACTGTGCTCAAGTGTGATCAAGTGTGATCAAGTGTGATCA 730  
DB 658 ACCTGACAGAGAGTGTGATCACTGTGCTCAAGTGTGATCAAGTGTGATCAAGTGTGATCA 717  
QY 731 CCTGCAATGTGTCCCGGAGTTTGAAGTGTGAGGCGCATCGGCGCTTGTGAGAGAGAGAG 790  
DB 718 CATGCAATGTGTCCCGGAGTTTGAAGTGTGAGGCGCATCGGCGCTTGTGAGAGAGAGAG 777  
QY 791 GGTGATCCCTTAAAGTCAACCGAGAGGCTGAGAGAGACTTCACTGTGTGTGAGAG 850  
DB 778 GACTGATACCTTGTGAGTGTGATCACTGAGAGAGGCGGAGAGAGTTCACCTCGGTGTGTGAG 837  
QY 851 AAATCATATGTATCATCTCTGTGCTTCTCAAGTGTGATCAAGTGTGATCAAGTGTGATCA 910  
DB 838 AAATCATATGTATCATCTCTGTGCTTCTCAAGTGTGATCAAGTGTGATCAAGTGTGATCA 897  
QY 911 ATTGCTACAGAAAGTGTCAAAAGCCGAGAGGCGAGCCCAAGAAACCGTGTGATCAAC 970  
DB 898 ATTGCTACAGAAAGTGTCTTAAGGCGAGAGAGGCGAGCAAGAGAAATCGTGTGATCAAC 957  
QY 971 TTGCCATCCCATCTGAGAACAGAGAACTCTGCGGTTCACAGTGTGAGAGAAAT 1022  
DB 958 TTGCTATCCCTTCAGAGAACAGAGAACTCTGTGTGTACTCTGTGAGAGAAAT 1009

RESULT 14  
AAC90601  
ID AAC90601 standard; cDNA; 645 BP.  
XX  
XX AAC90601;  
AC  
XX 13-MAR-2001 (first entry)  
XX  
XX Rat sodium channel beta3 protein Alrx94h5 partial coding sequence.  
DB  
XX Rat; sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;  
KM neurodegenerative disorder; mood disorder; muscle contraction; ss.  
XX  
XX Rattus sp.  
OS  
XX WO200069912-A1.  
PN 23-NOV-2000.  
XX  
XX 12-MAY-2000; 2000WO-US013144.  
PF  
XX 14-MAY-1999; 99US-0134198P.  
PR  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX Curtis RAJ;  
PI  
XX

DR WPI; 2001-122743/13.

XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal  
PT root ganglion cDNA library for use in chromosome mapping, forensic  
XX medicine, monitoring clinical trials and therapeutics.

PS Claim 1; Page 40-41; 145pp; English.

XX The present invention provides the protein and coding sequences of the  
CC rat sodium channel beta3 protein, designated Altra945. This protein is  
CC involved in the generation of pain and other sensory or perceptive nerve  
CC impulses, in the establishment and endurance of mood, neurodegenerative  
CC and sleep disorders, and in the control of muscle contraction, including  
CC movements such as the heartbeat, digestion and vascular tone. The  
CC sequences can be used in predictive medicine, screening and diagnostic  
CC assays, and in pharmacogenomics

SQ Sequence 645 BP; 155 A; 154 C; 181 G; 155 T; 0 U; 0 Other;

Query Match 42.4%; Score 534.6; DB 5; Length 645;  
Best Local Similarity 89.3%; Pred. No. 2e-133;  
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 376 ATGCTGCTTCAATAGATTTTCCCTGCTTCTCTGCTTATCTACTGCTCAGT 435  
Db 1 ATGCTGCTTCAATAGATTTTCCCTGCTTCTCTGCTTATCTACTGCTCAGT 60

QY 436 GTCTGCTTCTCTGCTTGTGTGAAGTCCCTCGAGACGAGCCGTGACGGCAATCC 495  
Db 61 GTCTGCTTCTCTGCTTGTGTGAAGTCCCTCGAGACGAGCCGTGACGGCAATCC 120

QY 496 ATGAGCTGGCTGCTCTCTGCTATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 555  
Db 121 ATGAGCTGGCTGCTCTCTGCTATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 180

QY 556 GAATGCTTCTACAGCCCGAGGCGGTAAAGATTTCTTTATTAACAGATTCGGAATGC 615  
Db 181 GATGCTTCTACAGCCCGAGGCGGTAAAGATTTCTTTATTAACAGATTCGGAATGC 240

QY 616 CACGAGAGGTGAG 675  
Db 241 CACGAGAGGTGAG 300

QY 676 CAGAGAGGTGAG 735  
Db 301 CAGAGAGGTGAG 360

QY 736 AATGTCCTCCGAG 795  
Db 361 AATGTCCTCCGAG 420

QY 796 ATCCCTTAAAGATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855  
Db 421 ATCCCTTAAAGATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

QY 856 ATGATGATCAATCTCTGCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 915  
Db 481 ATGATGATCAATCTCTGCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 916 TACAGAAAGGTCTCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 975  
Db 541 TACAGAAAGGTCTCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

QY 976 ATCCCATCTGAGAAACAAGAGAACTCTGCGGATCACTGAGAGAA 1020  
Db 601 ATCCCATCTGAGAAACAAGAGAACTCTGCGGATCACTGAGAGAA 645

RESULT 15  
AAV86895 standard; cDNA; 471 BP.  
XX ID AAV86895 standard; cDNA; 471 BP.  
XX AC AAV86895;

XX 27-APR-1999 (first entry)  
XX EST clone BM4.

XX Expressed sequence tag; secreted protein; haematopoiesis regulator;  
XX tissue growth; actinin; inhibin; tumour invasion suppressor; EST; human;  
XX chemotaxis; chemokinesis; hemostasis; gene therapy; thrombolysis;  
XX receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

OS Homo sapiens.

PN M09845435-A2.

PD 15-OCT-1998.

PF 10-APR-1998; 98MO-US006954.

PR 10-APR-1997; 97US-00835913.

PA (GENM) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Werberg D, Treacy M;

PI Spaulding V, Agostino MJ;

DR WPI; 1999-070076/06.

XX New polynucleotides encoding human secreted proteins - derived from e.g.  
PT human blood, kidney, foetal lung, placenta, testes, brain, ovary,  
PT pituitary, retina and colon cDNA libraries.

PS Claim 1; Page 383-384; 633pp; English.

XX This sequence represents an expressed sequence tag (EST), and is a  
CC polynucleotide of the invention. The polynucleotides of the invention are  
CC all secreted EST sequences isolated from a variety of human tissue  
CC sources. The EST sequences and proteins encoded by them are predicted to  
CC have useful biological activities which would make them suitable for  
CC treating, preventing or ameliorating medical conditions in humans and  
CC animals, although no supporting data is given. Suggested activities  
CC include nutritional activity, immune stimulating or suppressing activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC actinin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition  
CC activity. The EST sequences are also stated to be useful for gene therapy  
XX

SQ Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 0 U; 1 Other;

Query Match 34.0%; Score 429; DB 2; Length 471;  
Best Local Similarity 99.5%; Pred. No. 4.7e-105;  
Matches 440; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 369 CCAAG 428  
Db 22 CCAAG 81

QY 429 GGTGAGTGTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488  
Db 82 GGTGAGTGTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 140

QY 489 CAACCCCAAG 548  
Db 141 CAACCCCAAG 200

QY 549 GGTGAGTGTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608  
Db 201 GGTGAGTGTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260

QY 609 GAATGSCCAACAG 668  
Db 261 GAATGSCCAACAG 320

OY	669	GGACCTGCAGACGTGTCCATCCTGTGCTCAACGTCACTGTGAACGACTGTGGCTCTA	728
Db	321	GGACCTGCAGACGTGTCCATCCTGTGCTCAACGTCACTGTGAACGACTGTGGCTCTA	380
OY	729	CACCTGCATGTGTCCCGGAGTTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGAC	788
Db	381	CACCTGCATGTGTCCCGGAGTTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGAC	440
OY	789	GGGCTGATCCCCCTAAGATC	810
Db	441	GGGCTGATCCCCCTAAGATC	462

Search completed: April 1, 2005, 19:02:57  
 Job time : 767 secs

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OW nucleic - nucleic search, using SW model

Run on: April 1, 2005, 18:37:20 ; Search time 245 Seconds

(without alignments)  
8421.816 Million cell updates/sec

Title: US-09-977-579-4

Perfect score: 1261  
Sequence: 1 cctccctccgcagctcagc.....tgcacagactgagagccgcg 1261

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents NA: \*  
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2: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/6C COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143.8	11.4	617	4 US-09-949-016-2369	Sequence 2369, Ap
2	51	4.0	11174	4 US-09-949-016-1411	Sequence 1411, A
3	48.6	3.9	30337	4 US-09-949-016-13053	Sequence 13053, A
4	45.4	3.6	1645	4 US-09-023-587A-5	Sequence 5, Appl1
5	44.8	3.6	1053	4 US-09-902-540-2666	Sequence 2666, Ap
6	44.8	3.6	11558	5 PCT-US93-06251-23	Sequence 23, Appl1
7	44.8	3.6	13706	4 US-09-902-540-1124	Sequence 1124, Ap
8	42.4	3.4	2133	4 US-09-902-540-4106	Sequence 4106, Ap
9	42.4	3.4	23738	4 US-09-902-540-1203	Sequence 1203, Ap
10	42	3.3	9632	4 US-09-949-016-15003	Sequence 15003, A
11	41.6	3.3	636	4 US-09-469-039A-3591	Sequence 3591, A
12	40.6	3.2	2943	4 US-09-902-540-3929	Sequence 3929, Ap
13	40.6	3.2	21295	4 US-09-902-540-1194	Sequence 1194, Ap
14	40.4	3.2	1533	4 US-09-902-540-7877	Sequence 7877, Ap
15	40.4	3.2	5228	4 US-09-902-540-789	Sequence 789, Ap
16	40.4	3.2	6651	4 US-09-902-540-4944	Sequence 4944, Ap
17	40.4	3.2	30780	4 US-09-902-540-1243	Sequence 1243, Ap
18	40.2	3.2	2802	4 US-09-949-016-1335	Sequence 1335, Ap
19	40.2	3.2	2806	4 US-09-688-1888-102	Sequence 102, App
20	40.2	3.2	2806	4 US-09-291-417D-102	Sequence 102, App
21	40.2	3.2	2838	4 US-09-949-016-794	Sequence 794, App
22	40.2	3.2	57559	4 US-09-949-016-13077	Sequence 13077, A
23	40.2	3.2	57560	4 US-09-949-016-12536	Sequence 12536, A
24	39.2	3.1	601	4 US-09-949-016-124631	Sequence 124631, A
25	39.2	3.1	732	4 US-09-902-540-3806	Sequence 3806, Ap
26	39.2	3.1	6202	4 US-09-774-528-120	Sequence 120, App
27	39.2	3.1	8374	4 US-09-949-016-15257	Sequence 15257, A

C	28	39.2	3.1	18551	4 US-09-902-540-1187	Sequence 1187, Ap
C	29	39.2	3.1	45225	4 US-09-949-016-12428	Sequence 12428, A
C	30	39.2	3.1	45226	4 US-09-949-016-13654	Sequence 13654, A
C	31	39	3.1	30635	4 US-09-949-016-16501	Sequence 16501, A
C	32	39	3.1	43414	4 US-09-949-016-16501	Sequence 12839, A
C	33	39	3.1	43415	4 US-09-949-016-16491	Sequence 16491, A
C	34	38.8	3.1	1941	4 US-09-902-540-4762	Sequence 4762, Ap
C	35	38.8	3.1	26492	4 US-09-902-540-1234	Sequence 1234, Ap
C	36	38.6	3.1	513	4 US-09-902-540-8812	Sequence 8812, Ap
C	37	38.6	3.1	1407	4 US-09-902-540-6215	Sequence 6215, Ap
C	38	38.6	3.1	1940	4 US-09-718-032-1	Sequence 1, Appl1
C	39	38.6	3.1	1941	3 US-09-082-737-1	Sequence 1, Appl1
C	40	38.6	3.1	2310	4 US-09-774-528-142	Sequence 142, Appl1
C	41	38.6	3.1	6242	4 US-09-949-016-16490	Sequence 16490, A
C	42	38.6	3.1	8122	4 US-09-902-540-937	Sequence 937, App
C	43	38.6	3.1	13332	4 US-09-902-540-1047	Sequence 1047, App
C	44	38.6	3.1	32495	4 US-09-949-016-14952	Sequence 14952, A
C	45	38.4	3.0	505	4 US-09-621-976-15639	Sequence 15639, A

#### ALIGNMENTS

```
RESULT 1
US-09-949-016-2369
; Sequence 2369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2369
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2369

Query Match      11.4%; Score 143.8; DB 4; Length 617;
Best Local Similarity 56.9%; Pred. No. 36-31;
Matches 334; Conservative 0; Mismatches 232; Indels 21; Gaps 3;

QY 441 CTTCCCTGTGTGTGTGAAGTCCCTCGAGACGAGCCGTCAGAGCAACCCATGAA 500
DB 11 CTCGGGGGGGTGTGTGTGAAGTGTGACGACGAGCCGCTGTATGATGATCA 70
QY 501 GCTCCGCTGATCTCTCATGAAGAGAGAGAGGTGAGGCCACCAAGCTGTGAATG 560
DB 71 AATTCCTTTGATCTCTCGACGAGCCGCGAGACCAAGCTGTGAAGCTTCA 130
QY 561 GTTCTACAGCCGAGAGGGGGGTAAAGTT-----TCCTATTATGAGATGGAA 611
DB 131 GACCTTCGCGACAGAGGCACTGAGAGTTTCAAGATCTCGCTATGAGATGAGT 190
QY 612 TGGCCACCAAGAGAGTGAAGCCCTTTGAGAGGGCCCTGCAAGTGAATGCGAG----- 665
DB 191 GTTCGAGCTGTGAGAGAGATGAGCGCTTCGAGGGCCGCGTGTGATGAGCGCGGGG 250
QY 666 ---CAAGACCTGAGAGAGTGTCACTCACTGTCTCAAGCTCACTTGAAGCACTCTG 722
DB 251 CACCAAGACCTGAGAGATGTGTCTATCTTCATCAACCAATGCTACCAACCACTCGGG 310
QY 723 CCTTACACTGTGAATGTGTCCCGGAGATTGAGTTGAGGGGCAATCGGCTTTGTGAA 782
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Db 311 CCACTACAGAGTCCACGCTCTACCGCTGCTTTCTTCGAAAACACTACGACACACACG 370  
Qy 763 GACGAGCGGGGCTGATTCCTCCCTTAAGAGTACCCAGAGAGGTGAGAGACTTACCTCTGT 842  
Db 371 CGTCCTCAAGAGATCCATTTGAGGTAGTGAACAAAGCAACAGAGATGACATCCAT 430  
Qy 843 GGTCTCAGAAATCATGATGATGATCATCTTCTGCTTCTTCACCTGTGGCTGCTCATCGA 902  
Db 431 CGTCTCTAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490  
Qy 903 GATGATATATTGCTCAAGAGAGGTCTCAAAAGCCGAGAG--GAGCCCAAGAAAGCG 959  
Db 491 GATGATTTACTGCTCAAGAGAGATGCTGCCCGCCAGAGAGATGCTGACAGAGAAATGC 550  
Qy 960 GCTGACTACCTTGCATCCCATCTGAGAGCAAGAGAACTGTGGG 1006  
Db 551 CTCGGAATATCTGGCCATCATCTTGAAAGCAAGAGAACTGCACGG 597

## RESULT 2

US-09-949-016-14111  
; Sequence 14111, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 14111  
; LENGTH: 11174  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(11174)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14111

Query Match 4.0%; Score 51; DB 4; Length 11174;  
Best Local Similarity 58.1%; Pred. No. 0.00076;  
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 441 CTTCCCTGTGTGTGTGAAGTCCCTCGAGAGCGAGCGCTGACGGCAACCCATGAA 500  
Db 2011 CTGCGGGGGCTGCTGAGAGTGAAGTCCGAGACCGAGCGCGTGTATGAGATACCTTCA 2070  
Qy 501 GGTGGGCTGATCTCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560  
Db 2071 AATTCCTTTCATCTCTGCAAGCGCGCGAGCGAGCAACAGCTTGAAGACCTTCA 2130  
Qy 561 GTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTA 595  
Db 2131 GACCTTCCGCCAGAGGGGACTGAGAGATTGTCA 2165

## RESULT 3

US-09-949-016-13053  
; Sequence 13053, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 13053  
; LENGTH: 30337  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(30337)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13053

Query Match 3.9%; Score 48.6; DB 4; Length 30337;  
Best Local Similarity 63.0%; Pred. No. 0.0062;  
Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 829 GACTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888  
Db 620 GACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679  
Qy 889 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 947  
Db 680 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 738

## RESULT 4

US-09-023-587A-5  
; Sequence 5, Application US/09023587A  
; Patent No. 6653530  
; GENERAL INFORMATION:  
; APPLICANT: Shewmaker, Christine K.  
; APPLICANT: Bhat, Ganesh B.  
; APPLICANT: Venkatramesh, Mylavaram  
; APPLICANT: Rangwala, Shaikat H.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Boddupalli, Sekhar S.  
; TITLE OF INVENTION: Methods for Producing Carotenoid Compounds, Tocopherol Compounds,  
; FILE REFERENCE: 16516.122  
; CURRENT APPLICATION NUMBER: US/09/023,587A  
; CURRENT FILING DATE: 1998-02-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 5  
; LENGTH: 1645  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-023-587A-5

Query Match 3.6%; Score 45.4; DB 4; Length 1645;  
Best Local Similarity 46.2%; Pred. No. 0.012;  
Matches 151; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 429 GGTAGTGTCTGCTTCCCTGT 488  
Db 349 GGTGTCTCAAGCGCTCTTCTTAAGGTACAGAGCGCCCAAGAGCGCTGTACGT 408  
Qy 489 CAACCCATGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548  
Db 409 GGTGCTACCAACACTGACAGCGGAGCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 468  
Qy 549 GGTGTGGAATGTGTTCTTACAGAGCGCGGTAAAGATTCTTATTATTCAGAGTATCG 608

DB 469 CGAGTGAACGCGATCGTGGGCGCGAGCGCCCAACTCTCGGTGGCCAACGATGGG 528  
QY 609 GAATGCCACCCAGAGAGTGAAGAGCCCTTTCAGAGGGCGCGCTGAGTGAATGGACCA 668  
DB 529 CGGGGCGATACGAGTACGCGCATCGGTTCAGAGGCGCGGTCAAGATCCCGACGACAA 588  
QY 669 GGACCTGCAAGAGAGTGTCCATCACTGTGCTCAAGCTCACTGAGAGTCTGGCCCTCTA 728  
DB 589 GATGTGTACTACGAGAGAGGCGCGAGATGTATGTCGTGGGAGACGCTCTCTCCGACTT 648  
QY 729 CACTGCAATGTGTCCCGGAGTTTGA 755  
DB 649 CTACGGCTGGGTGTCTCCCAAGTGA 675

RESULT 5  
US-09-902-540-2666  
; Sequence 2666, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 2666  
; LENGTH: 1053  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; US-09-902-540-2666

Query Match 3.6%; Score 44.8; DB 4; Length 1053;  
Best Local Similarity 52.1%; Pred. No. 0.014;  
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 436 GTCGCTTCCCTGTGTGTGAAGTCCCTCGAGAGCGAGCGCGTGCAGGCAACCC 495  
DB 151 GACTTCTCCACGAGACCTGCTGACCTGCGCTCGAAGATGACGAGCGGAGCGCCACTC 210  
QY 496 ATGAAGCTGCGTGCATCTCTGATGAAGAGAGAGAGGTGAGGCGCACCGGTGTG 555  
DB 211 ATCCACCGGCTGTGCGTCTTTCGCGACGGGTGACGATCGTGGCAACAACCTGTG 270  
QY 556 GAATGTTCTACAGCGCCCGAGGGCGGTAAAGATTCTTATTCAGATTCGGAATGC 615  
DB 271 CTGAACCTTACAGACCTGAAGCGCCCTGAGCGCGGATGTACTGTGCGCCAGCTC 330  
QY 616 CACGAGAGGTG 627  
DB 331 TACGAGAGGCG 342

RESULT 6  
PCT-US93-06251-23  
; Sequence 23, Application PC/TUS9306251  
; GENERAL INFORMATION:  
; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06251  
FILING DATE: 19930630  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Digilio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 8586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11558 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-23

Query Match 3.6%; Score 44.8; DB 5; Length 11558;  
Best Local Similarity 56.7%; Pred. No. 0.048;  
Matches 102; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 74 GGGGTGGGCGGGAGGCGAAGTGTCCGTGTGCTGAGCGCGCGGAGCGGGCGGAGC 133  
DB 428 GGGAGGGGCGGGTGGAGGACCTTTCAGAGCAGAGAGGCTTTTGGGGCGTGGCGCGC 487  
QY 134 GCGTGTGCGCTCTCTGAACTGGGAGGTCCAGTGGGTG-CTTAGGCGCCAAAGCCC 192  
DB 488 TGCAGAGCGGAGCGGGCTGACGCGGTGCGCTGCGCGCGAGTGTATGACAGCGCGC 547  
QY 193 CCACCGGCTCCAAAGCTTCCAGGGCTTCCAGAGCAGGTGCTGCGGCTTCTTCG 252  
DB 548 CCGGCCGGAACCCCGAGCGCGCGGGCTCCACCCGCGGCTCCCGCCCTCCCGCG 607

RESULT 7  
US-09-902-540-1124/C  
; Sequence 1124, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1124  
; LENGTH: 13706  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; US-09-902-540-1124

Query Match 3.6%; Score 44.8; DB 4; Length 13706;  
Best Local Similarity 52.1%; Pred. No. 0.052;  
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 436 GTCGCTTCCCTGTGTGTGAAGTCCCTCGAGAGCGAGCGCGTGCAGGCAACCC 495  
DB 4948 GACTTCTCCACGAGACCTGCTGACCTGCGCTCGAAGATGACGAGCGCGACCACTC 4889

Oy	496	ATGAAGCTGGCCTGATCTCCGTCAATAAAGAAGAGAGGGAGGAGGCCACACCGTGTGTG	555
Db	4888	ATCACCCGGCGTGTCGTCGTTCTTCGCACGGGTGAACAATCTGTCGCAACAACCTGGTGTG	4822
Oy	556	GATGTGTTCTACAGGCCCGGAGGGCGGGTAAGAATTCTTATTTACAGATTCGAAATGAC	615
Db	4828	CTGAACCTCTTACAAAGCACCTTAATCCCCCTGAAGCGCGGAATGACTCTGTGGCCAAGCTC	4765
Oy	616	CACCAGAGAGTG	627
Db	4768	TACGAGAGGCG	4757

```

RESULT 8
US-09-902-540-4106/c
; Sequence 4106, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4106
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-4106

```

Query Match	3.4%	Score 42.4	DB 4	Length 2133
Best Local Similarity	51.6%	Pred. No. 0.1		
Matches	97	Conservative	0	Mismatches 91; Indels 0; Gaps 0
QY	462	GCCCTCGAGACGAGGCCGTCGACAGGCAACCCCATGAAGCTGCGTCGATCTCTGCAT	521	
Db	1813	GGCCACAGATGATGCGGGCGCGCCATCCCGTTTCGAAAGACGCGTCGACACCGGCCCTGCAAG	1754	
QY	522	GAAAGAAAGAGAGGTGAGGCGCACACAGGTGTAATGTTCTACAGAGCCCGAAGGCGG	581	
Db	1753	GAAAGCGGCGCGAGTCGAGACACCTGAGCGTGGACCCGCTTCCAGACACAGTGTGCT	1699	
QY	582	TAAAGATTTCCTTATTTACGATATCGAATATGCGCACACGAGAGGTGAGAGGCCCTTTCA	641	
Db	1693	GAGTGAACGCTCCGCTACGAGGATCTTCGCGGACCTCCAGCTCGGACAGCGCGCGGTGCA	1633	
QY	642	GGGGCGCC	649	
Db	1633	GCTCGCG	1626	

```

RESULT 9
US-09-902-540-1203
: Sequence 1203, Application US/09902540
: Patent No. 6833447
: GENERAL INFORMATION:
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: APPLICANT: Wiegand, Roger C.
: TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
: FILE REFERENCE: 38-10(15849)B
: CURRENT APPLICATION NUMBER: US/09/902,540
: CURRENT FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: 60/017,883
: PRIOR FILING DATE: 2000-07-10
: NUMBER OF SEQ ID NOS: 16825
: SEQ ID NO 1203

```

```

; LENGTH: 23738
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1203

```

Query Match	3.4%	Score 42.4;	DB 4;	Length 23738;
Best Local Similarity	51.6%	Pred. No. 0.34;		
Matches 97;	Conservative 0;	Mismatches 91;	Indels 0;	Gaps 0;

QY	462	GCCTTCGAGACGAGGCGCGGACAGGCAACCCCATAGAGTTCGCGATCTCTGCAT	521
Db	4191	GGCCAGATATATGCGCGGCGCGCCATCCCTTCGAAACGCGTGCACACGCGCCGTGCAG	4250
QY	522	GAAGAGAGAGAGGTGAGGCCACACGCGTGTGGAAATGTTTCAAGGCCCGAGGCGG	581
Db	4251	GAATCGGCGCGCGGAGATCGAGCACGCTGGGCGTGGACCGCTTCCAGACACAGATGTCGT	4310
QY	582	TAAAGATTTCTTATTTTACAGATATCGGAATGCGCACAGAGAGTGGAGAGAGCCCTTTCA	641
Db	4311	GGGTGAAGCGCTTCGATCGACGAGATTCGCGGAGACTCGAGTTCGAGACAGCCCGCGTGA	4370
QY	642	GGGCGGCC	649
Db	4371	GCTCCGCC	4378

```

RESULT 10
US-09-949-016-15003/c
; Sequence 15003, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15003
; LENGTH: 9622
; TYPR: DNA
; ORGANISM: Human
US-09-949-016-15003

```

Query Match	3.3%	Score 42	DB 4	Length 9622
Best Local Similarity	49.5%	Pred. No. 0.28		
Matches 108	Conservative 0	Mismatches 110	Indels 0	Gaps 0
Qy	38	GAGCGAGGACAGGGGCGCGATGTGAAGCTGAGATTCGGGGGTGGGCGGGAGGCGACTGTGC	97	
Db	7138	GCGTAGAGCCCTCGCTGTGAAGGGGTCGCTGCTGCACCGTAGGGGCTCTGTTCCATGGCCACGA	7079	97
Qy	98	CGTGGTGTGAAGCCGCCCGGACGAGCCGGGCGGGAGCGGGATGTGGGTCTCCCTCGAATCGG	157	
Db	7078	TCTGCTCTGTGTGGGGGCGCAGCGGCGGTGTAAGAAAGCAATCATCCCTCCATGCGGCTGG	7019	157
Qy	158	GGAGGTCCAGTGGGGGTGCGCTTAGGGGCCCAAAAGCCCCACCCGAGCTCCAAAAGCTCCGAG	217	
Db	7018	ACAGGAACCTCTGGGGGGACAGTAGAGCTTCAACCCCTTGAGCTGTCCAGCGCTTCCAGC	6959	217
Qy	218	GCCTCCCGACGACCGGTGCTCGGCGCCCTTCCTTGGATC	255	
Db	6958	TACACCCGACGAGCTCCCTTCTGTATCTCTTGGAGC	6921	255



US-09-489-039A-3591  
; Sequence 3591, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 3591  
; LENGTH: 696  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-3591

Query Match 3.3%; Score 41.6; DB 4; Length 696;  
Best Local Similarity 48.3%; Pred. No. 0.098;  
Matches 116; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 458 AAGTGCCTTCGAGACGAGCGCGTCGAGGCAACCCCATGAGCTGCTGATCTCT 517  
DB 92 AGCGCGCGACGTCGCGCAGCGCGTGTGCAAGCTGCCGAGCCGCGCTATGCGACT 151  
QY 518 GCATGAGAGAGAGAGGTGAGAGCCACCGTGTGTAATGTTCTACAGCCCGAGG 577  
DB 152 ACCTGCGCTTCAACGAGTTCGAGGTAACCCGCTGATTCAGGGAATTCGCTGTGTTCC 211  
QY 578 GCGGTAAGATTCTTATTATTCAGATTCGAAATGGCCACGAGAGGTGAGAGCCCT 637  
DB 212 CCGGCGCGAATCTTTCATCCGAGAGATGTCTTACGCTGACGAGCGCGCGCCGG 271  
QY 638 TTCAGGCGCGCTGACGTGAAATGACGACGACCTGACGAGCGTGTCCATCATGTGC 697  
DB 272 TCATCTCGACCTGCTTAAAGTATTCGACCCGCGCGCGCTGCGCATGCGCAGGC 331

RESULT 12  
US-09-902-540-3929  
; Sequence 3929, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 3929  
; LENGTH: 2943  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-3929

Query Match 3.2%; Score 40.6; DB 4; Length 2943;  
Best Local Similarity 48.9%; Pred. No. 0.39;  
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 460 GTGCCCTCGAGACGAGCGCGTCGAGGCAACCCCATGAGCTGCTGATCTCTGC 519  
DB 1831 GTGCTGGAAGAGGTGAGGCGCGCTGCGCAGCTGAGCTGATGCGCGCAGAGCCCG 1890  
QY 520 ATGAAGAGAGAGGTGAGGCGCACCGTGTGTAATGTTCTACAGCCCGAGGCG 579  
DB 1891 ATGGCTTACGCGCAGAGCTGAAGGCGCGGTGAGAGCGCGCGCGCCACGATGAAGCGC 1950

QY 580 GGTAAAGATTCTTATTACGAGTATCGGAATGGCCACGAGAGGTGAGAGCCCTT 639  
DB 1951 GCCTATGACCCGCTCTCGAGCGTGGCAGCTTTCAGCCGCGCGCGGTGAGCGCTGTG 2010  
QY 640 CAGGCGCGCTGACGTGATGAGCAGCAGCAGCCTGACGAGC 682  
DB 2011 AAGCGCGCCAGAGAGGCAATGAGCATGAGCGCGCAGAGAGG 2053

RESULT 13  
US-09-902-540-1194  
; Sequence 1194, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1194  
; LENGTH: 21295  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-1194

Query Match 3.2%; Score 40.6; DB 4; Length 21295;  
Best Local Similarity 48.9%; Pred. No. 1.1;  
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 460 GTGCCCTCGAGACGAGCGCGTCGAGGCAACCCCATGAGCTGCTGATCTCTGC 519  
DB 2609 GTGCTGGAAGAGGTGAGGCGCGCTGCGCAGCTGAGCTGATGCGCGCAGAGCCCG 2668  
QY 520 ATGAAGAGAGAGGTGAGGCGCACCGTGTGTAATGTTCTACAGCCCGAGGCG 579  
DB 2669 ATGCGCTTACGCGCAGAGCTGAAGCGCGCGGTGAGCGCGCGCCACGATGAAGCGC 2728  
QY 580 GGTAAAGATTCTTATTACGAGTATCGGAATGGCCACGAGAGGTGAGAGCCCTT 639  
DB 2729 GCCTATGACCCGCTCTCGAGCGTGGCAGCTTTCAGCCGCGCGGTGAGCGCTGTG 2788  
QY 640 CAGGCGCGCTGACGTGATGAGCAGCAGCCTGACGAGC 682  
DB 2789 AAGCGCGCCAGAGAGGCAATGAGCATGAGCGCGCAGAGAGG 2831

RESULT 14  
US-09-902-540-7877  
; Sequence 7877, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 7877  
; LENGTH: 1533  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus

US-09-902-540-7877

Query Match 3.2% Score 40.4; DB 4; Length 1533;  
Best Local Similarity 47.9%; Pred. No. 0.32;  
Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 607 CGGAATGGCCACAGAGAGTGGAGAGCCCTTTTCAGGGGCGCTGACGTGAATGGACAGC 666  
DB 310 CGGATGCCCCGAGACAGTGTGCTCCGAGGAGGGGCTGTCTGGGGATGGGGAC 369  
QY 667 AAGAACCTGCAGAGAGTGTCCATCACTGTGCTCAACGTCACTTGAACGACTTGGCCTC 726  
DB 370 ACGGAGCTGCAGAGACTGTGGCGCGGTAACAGGTGAACCGGCTGGGTCCACGTGGGC 429  
QY 727 TACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTGTGAAGAG 786  
DB 430 TTGACCCGCAACCCATCCGCTGTGGCTCTGTGAAGGGGCGCTGGCGAAGTGGGCAATCAC 489  
QY 787 ACGCGGCTGATCCCTTAAGATCAACGAGAGGCTGAGAGGACTTCACTTGTGGTC 846  
DB 490 GTGCTGTGCGGCTCTGTCTTCAACCGGGGCGCTTCTGTGTCAGCGGCGCATCGTG 549  
QY 847 TC 848  
DB 550 TC 551

## RESULT 15

US-09-902-540-789  
; Sequence 789, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 789  
; LENGTH: 5228  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-789

Query Match 3.2% Score 40.4; DB 4; Length 5228;  
Best Local Similarity 47.9%; Pred. No. 0.6;  
Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 607 CGGAATGGCCACAGAGAGTGGAGAGCCCTTTTCAGGGGCGCTGACGTGAATGGACAGC 666  
DB 3057 CGGATGCCCCGAGACAGTGTGCTCCGAGGAGGGGCTGTCTGGGGATGGGGAC 3116  
QY 667 AAGAACCTGCAGAGAGTGTCCATCACTGTGCTCAACGTCACTTGAACGACTTGGCCTC 726  
DB 3117 ACGGAGCTGCAGAGACTGTGGCGCGGTAACAGGTGAACCGGCTGGGTCCACGTGGGC 3176  
QY 727 TACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTGTGAAGAG 786  
DB 3177 TTGACCCGCAACCCATCCGCTGTGGCTCTGTGAAGGGGCGCTGGCGAAGTGGGCAATCAC 3236  
QY 787 ACGCGGCTGATCCCTTAAGATCAACGAGAGGCTGAGAGGACTTCACTTGTGGTC 846  
DB 3237 GTGCTGTGCGGCTCTGTCTTCAACCGGGGCGCTTCTGTGTCAGCGGCGCATCGTG 3296  
QY 847 TC 848  
DB 3297 TC 3298

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Job time : 252 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 20:37:33 ; Search time 816 Seconds  
(without alignments)  
9353.177 Million cell updates/sec

Title: US-09-977-579-4

Perfect score: 1261  
Sequence: 1 cccctccctccgagctgagc.....tgccagagactgagagccgcg 1261

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 3: /cgn2\_6/prodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 4: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 12: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 13: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 16: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 17: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 18: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 19: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 20: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 21: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*
- 22: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1261	100.0	1261	US-09-977-579-4	Sequence 4, Appl
2	559.6	44.4	2632	US-10-029-191-22	Sequence 22, Appl
3	559.6	44.4	3108	US-10-029-191-1	Sequence 1, Appl
4	540	42.8	2220	US-09-977-579-3	Sequence 3, Appl
5	534.6	42.4	645	US-10-029-191-21	Sequence 21, Appl
6	216	17.1	4635	US-09-764-891-7659	Sequence 7659, Ap
7	148.2	11.8	657	US-10-029-191-23	Sequence 23, Appl
8	143.8	11.4	1335	US-10-723-860-2247	Sequence 2247, Ap
9	142.2	11.3	1414	US-10-477-721-1	Sequence 1, Appl
10	141	11.2	407	US-10-276-774-718	Sequence 718, Ap
11	138.6	11.0	1490	US-09-917-800A-1654	Sequence 1654, Ap

12	81.4	6.5	807	US-10-401-916-12	Sequence 12, Appl
13	81.4	6.5	974	US-10-401-916-13	Sequence 13, Appl
14	49	3.9	243	US-10-029-386-16214	Sequence 16214, A
15	49	3.9	569	US-10-029-386-2514	Sequence 2514, Ap
16	48.6	3.9	3583	US-10-723-860-6471	Sequence 6471, Ap
17	45.4	3.6	876	US-10-767-701-10747	Sequence 10747, A
18	45.2	3.6	497	US-10-424-599-133788	Sequence 133788,
19	45.2	3.6	954	US-10-425-115-100998	Sequence 100998,
20	44.8	3.6	921	US-10-369-493-43050	Sequence 43050, A
21	44.8	3.6	29340	US-10-322-281-642	Sequence 642, App
22	43.8	3.5	1434	US-10-259-194A-622	Sequence 622, App
23	43.8	3.5	1720	US-10-425-114-15213	Sequence 15213, A
24	43.8	3.5	1764	US-10-425-114-15538	Sequence 15538, A
25	43.8	3.5	1794	US-10-425-114-25057	Sequence 25057, A
26	43.8	3.5	2029	US-10-425-115-15884	Sequence 15884, A
27	43	3.4	386	US-10-437-963-98256	Sequence 98256, A
28	43	3.4	1021	US-10-767-701-11876	Sequence 11876, A
29	42.8	3.4	1298	US-10-437-963-21288	Sequence 21288, A
30	42.6	3.4	419	US-10-425-115-24179	Sequence 24179, A
31	42.2	3.3	1211	US-10-437-963-27585	Sequence 27585, A
32	41.6	3.3	1362	US-10-282-122A-23492	Sequence 23492, A
33	41.4	3.3	686	US-10-437-963-90177	Sequence 90177, A
34	41.4	3.3	58038	US-10-741-600-17942	Sequence 17942, A
35	41.4	3.3	333811	US-10-741-600-17681	Sequence 17681, A
36	41.2	3.3	922	US-10-017-161-1435	Sequence 1435, Ap
37	41.2	3.3	922	US-10-292-798-1161	Sequence 1161, Ap
38	41	3.3	1097	US-09-771-161A-58	Sequence 58, Appl
39	41	3.3	3382	US-09-771-161A-59	Sequence 59, Appl
40	40.6	3.2	221000	US-10-174-014-12	Sequence 12, Appl
41	40.6	3.2	23380	US-10-087-192-652	Sequence 652, App
42	40.2	3.2	766	US-10-260-238-52	Sequence 52, Appl
43	40.2	3.2	779	US-10-425-114-26163	Sequence 26163, A
44	40.2	3.2	791	US-10-437-963-84059	Sequence 84059, A
45	40.2	3.2	1071	US-10-437-963-84064	Sequence 84064, A

ALIGNMENTS

RESULT 1  
US-09-977-579-4  
; Sequence 4, Application US/09977579  
; Publication No. US20040248240A1  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge University Technical Services  
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi  
; TITLE OF INVENTION: channel  
; FILE REFERENCE: 674558-2001  
; CURRENT APPLICATION NUMBER: US/09/977,579  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP00/01783  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60,129,473  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1261  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-977-579-4

Query Match 100.0%; Score 1261; DB 11; Length 1261;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTCTCCCTCCGAGCTGAGCTTACCTCTGCGGAAACGAGCGGAGCGGCGGAGTGG 60  
DB 1 CCTCTCCCTCCGAGCTGAGCTTACCTCTGCGGAAACGAGCGGAGCGGCGGAGTGG 60  
QY 61 AACCTGAGTTCGCGGAGTGGCGGAGGAGCGAGTCTCGTGTGCTGAGCGCGGAGAGA 120

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Db 61 AAGCTGAGATTCGGGGGTGGGGGAGGCGAATGCTCCGTGCTGAGCGCGCGAGA 120
Qy 121 GGGGGGGGGAGCGGCTGATGGGCTCCCTCGAATGGGGAGGTCAGTGGGGTGGCTTAC 180
Db 121 GGGGGGGGGAGCGGCTGATGGGCTCCCTCGAATGGGGAGGTCAGTGGGGTGGCTTAC 180
Qy 181 GGGCCAAAGCCCCCAGCCCGGCTCAAAAAGCTCCAGGGCTCCAGAGGACCGGTGCTCG 240
Db 181 GGGCCAAAGCCCCCAGCCCGGCTCAAAAAGCTCCAGGGCTCCAGAGGACCGGTGCTCG 240
Qy 241 GCGCTTCTTGGGTGAGAAAGTGGCCCTGGGGGAGTTCGTCCCAAGGGTTCTCTCG 300
Db 241 GCGCTTCTTGGGTGAGAAAGTGGCCCTGGGGGAGTTCGTCCCAAGGGTTCTCTCG 300
Qy 301 AAAGAAATCGAGAGGGCGAGTCCCTGACCGAGGGAATCTCTGTGTAGACTTGGAAAGC 360
Db 301 AAAGAAATCGAGAGGGCGAGTCCCTGACCGAGGGAATCTCTGTGTAGACTTGGAAAGC 360
Qy 361 CGCCAGCCCCAGAAAGATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTCTG 420
Db 361 CGCCAGCCCCAGAAAGATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTCTG 420
Qy 421 ATCTACTGGGTCAAGTGTCTGCTTCCCTGTGTGTGTGAAAGTGCCTCGAGAGCGAGGCC 480
Db 421 ATCTACTGGGTCAAGTGTCTGCTTCCCTGTGTGTGTGAAAGTGCCTCGAGAGCGAGGCC 480
Qy 481 GTGCGAGGGAACCCGATGAGCTGAGCTGAGCTCTCTGATGAAGAGAGAGAGGTGAG 540
Db 481 GTGCGAGGGAACCCGATGAGCTGAGCTGAGCTCTCTGATGAAGAGAGAGAGGTGAG 540
Qy 541 GCCACCAAGGTGGTGAATGTTCTTACAGGCCCGAGGGCGGTAAAGATTTCTTATTTAC 600
Db 541 GCCACCAAGGTGGTGAATGTTCTTACAGGCCCGAGGGCGGTAAAGATTTCTTATTTAC 600
Qy 601 GAGTATCGGAATGGCCACCGAGAGGTGAGAGGCCCTTTAGGGGCGCTTGTGAGTAAT 660
Db 601 GAGTATCGGAATGGCCACCGAGAGGTGAGAGGCCCTTTAGGGGCGCTTGTGAGTAAT 660
Qy 661 GGCACCAAGGACCTGAGAGGCTGATCCCTTAAAGATCACTGATGCTCACTGTGAACAACCT 720
Db 661 GGCACCAAGGACCTGAGAGGCTGATCCCTTAAAGATCACTGATGCTCACTGTGAACAACCT 720
Qy 721 GGCCTCTTACCTGAGATGTGTCCCGGAGTTTGAATTTGAGGCGCATCGGCCCTTTG 780
Db 721 GGCCTCTTACCTGAGATGTGTCCCGGAGTTTGAATTTGAGGCGCATCGGCCCTTTG 780
Qy 781 AAGACGAGCGGCTGATCCCTTAAAGATCACTGAGAGGCTGAGAGGATCTTCACTCT 840
Db 781 AAGACGAGCGGCTGATCCCTTAAAGATCACTGAGAGGCTGAGAGGATCTTCACTCT 840
Qy 841 GTGTCTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 841 GTGTCTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Qy 901 GAGATGATATATTTGCTACAGAAAGTCTCAAAAAGCCGAGAGGACCCCAAGAAAACCG 960
Db 901 GAGATGATATATTTGCTACAGAAAGTCTCAAAAAGCCGAGAGGACCCCAAGAAAACCG 960
Qy 961 TCTGACTACTTGGCCATCCATCTGAGAAACAAGGAACTCTGCGGTACAGTGAAGAA 1020
Db 961 TCTGACTACTTGGCCATCCATCTGAGAAACAAGGAACTCTGCGGTACAGTGAAGAA 1020
Qy 1021 TAGAACAGAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 TAGAACAGAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Qy 1081 TTACAGCAATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
Db 1081 TTACAGCAATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
Qy 1141 ATTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1200
Db 1141 ATTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1200
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Qy 1201 GACTCCCTAATCTCATGACCTCTACGACCAATAGACTCTGCGAGAACTGAGAGCCG 1260
Db 1201 GACTCCCTAATCTCATGACCTCTACGACCAATAGACTCTGCGAGAACTGAGAGCCG 1260
Qy 1261 G 1261
Db 1261 G 1261

RESULT 2
US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00X/501
; CURRENT APPLICATION NUMBER: US/10/029.191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Query Match 44.4%; Score 559.6; DB 13; Length 2632;
Best Local Similarity 84.4%; Pred. No. 3.1e-163;
Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

Qy 371 AGAAGATGCTGCTGCTCAATGATGTTTCCCTGAGCTTCTCTGCTTACTACTGG 430
Db 73 AAAAGATGCTGCTGCTCAACAGATTTGCTTCCCTGAGCTTCTCTGCTTACTACTGG 132
Qy 431 TCAGTGTCTGCTTCCCTGCTGTGTGTGTGAAAGTCCCTCGAAGACGAGGCCGTGAGGCA 490
Db 133 TCAGAGTGTGCTTCCCTGTGTGTGTGTGAAAGTCCCTCGAAGACGAGGCCGTGAGGCA 192
Qy 491 ACCCATGAAGCTGGCTGCTATCTCTGCAATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 550
Db 193 ATCCATGAAGCTGAAGTGAATCTCTGCAATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 252
Qy 551 TGTGGAATGTTTCTACAGGCGCCGAGGCGGTAAAGATTTCTTATTTACAGATACGGA 610
Db 253 TGTGGAATGTTTCTACAGGCGCTGAGGCGGTAAAGATTTCTTATTTACAGATACGGA 312
Qy 611 ATGGCCACAGAGGTGAGAGAGCCCTTTTCAAGGGCGCTGCAATGAGAGAGAGAGAGAG 670
Db 313 ATGGCCACAGAGAGTGAAGAGAGCCCTTTTCAAGGGCGCTGCAATGAGAGAGAGAGAGAG 372
Qy 671 ACCCTGAGAGAGTGTCTATCTGTGTCTCAACGTCACTGTGAAGAGAGAGAGAGAGAGAG 730
Db 373 ACCCTGAGAGAGTGTCTATCTGTGTCTCAACGTCACTGTGAAGAGAGAGAGAGAGAGAG 432
Qy 731 CCTGCAATGTTGCTCCGGAGGTTTGAAGTGTGAGGCGATCGGCCCTTTTGAAGAGAGAGAG 790
Db 433 CATGCAATGTTGCTCCGGAGGTTTGAAGTGTGAGGCGATCGGCCCTTTTGAAGAGAGAGAG 492
Qy 791 GCGTGAATCCCTTAAGAGTCAACGAGAGGCTGAGAGAGAGTTCACCTGTGTGTTCTAG 850
Db 493 GACTGATACCTTTGGAGTCACTGAAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
Qy 851 AAATCATATGTAATCTCTTGTGTCTTCTTCAACCTGTGTGTGTGTGTGTGTGTGTGTGT 910
Db 553 AAATCATATGTAATCTCTTGTGTCTTCTTCAACCTGTGTGTGTGTGTGTGTGTGTGTGT 612
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QY 911 TTTCCTCAAGAAAGSTCTCAAAAGCCCAAGAGGACGCCCAAGAAAAGCGCTGATAC 970  
Db 613 ATTCTCAAGAAAGSTCTCTAAGGCCCAAGAGGACGCAAGAAAATCGCTGATAC 672  
QY 971 TTGCATCCCATCTGAGAACAAAGGAACTCTGCGGTACCAAGTGAGGAATAGAAACAGGA 1030  
Db 673 TTGCTATCCCTTCAGAGAAACAAGAGAACTCTGTGTATCTGTGGAGGAATA-----AT 726  
QY 1031 GCAGTGTGACATGAGGTGGGCTTGAAACACTAGGGACTGGACATCCATGTTTCAGCAATG 1090  
Db 727 GTGTGTGTGACTTGTAGTGTATCTG-AGTGTGAGGACTGTGATATCCCAAGTTCAGTGATG 785  
QY 1091 TCATGTGATAGAGAGGGGCGCCCAAGGGGCCCATGCGCTTCCCTCATGATTCAT 1146  
Db 786 CCAGCAATATAGGAATGTGCCCAAGGTGTCCCAACATTCATCTTTTCTATTCAT 841

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RESULT 3
US-10-029-191-1
: Sequence 1, Application US/10029191
: Publication No. US20020160453A1
: GENERAL INFORMATION:
: APPLICANT: CURTIS, ROY A.J.
: TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
: TITLE OF INVENTION: PROTEIN
: FILE REFERENCE: 210147.00XX/5U1
: CURRENT APPLICATION NUMBER: US/10/029,191
: CURRENT FILING DATE: 2001-12-20
: PRIOR APPLICATION NUMBER: 09/569,978
: PRIOR FILING DATE: 2000-05-12
: PRIOR APPLICATION NUMBER: US 66/134,198
: PRIOR FILING DATE: 1999-05-14
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 3108
: TYPE: DNA
: ORGANISM: Rattus bp.
US-10-029-191-1

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Query Match	44.4%	Score 559.6	DB 13	Length 3108
Best Local	84.4%	Pred. No. 3.3e-163		
Similarly				
Match 655	0	Mismatches 114	Indels 7	Gaps 2
Conservative				

QY	371	AGAAGATGCCGACCTTCAATAGATTTGTTCCCGGCTTCTCTGCTGTATCTATGCGG	430
Db	73	AAAGATGCTCCCTTCAACAGATTCTTCCCTTACCTTCTTATGCTCATCTATCTAGG	132
QY	431	TCAGTGTCTGCTTCCCTGTGTGTGTGGAAGTGCCCTCGAGAAGGAGCCGTGAGGCA	490
Db	133	TCAGAGTCTGCTTCCCTGTGTGTGTGGAAGTGCCCTCGAGAAGGAGCGGTGAGGCA	192
QY	491	ACCCCATGAACTGCGCTGCATCTTCTGCAATGAAGAGAGAGAGGTGAGGCGACACAGG	550
Db	193	ATCCCATGAACCTGAGTGTCATCTTCTGCAATGAAGAGAGAGAGGTGAGGCGACACTG	252
QY	551	TGTGTGAATGTTCTACAGAGCCCGAGGCGGTAAGATTTCTTATTTACAGATTCGGA	610
Db	253	TGTGTGAATGTTCTACAGAGCCCTGAGGCGGTAAAGATTTCTTATATATGATGATTCGA	312
QY	611	ATGSCCACCAGAGAGGTGAGAGCCCTTTCAGGGCGGCTCGACGTGAATGACAGCAAGG	670
Db	313	ATGSCCACCAGAGAGGTGAGAGCCCTTTCAGAGGCGGCTCGACGTGAATGAGGAGCAAG	372
QY	671	ACCTGACGAGAGTGTGCATCTACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTTACA	730
Db	373	ACCTGACGAGAGTGTGCATCTACTGTGCTCAACGTCACTCTGAATGACTCTGGCCTTACA	432
QY	731	CCTGCAATGTGTCCCGGAGTTTGAAGTTCGAGCGCATCGGCGCTTTGTGAAGACGACG	790
Db	433	CATGCAATGTGTCCAGGAGTTTGAATTCGAATTCAGAGCACAAGGCGCTTTTGTGAAGACGACA	492
QY	791	GCGTATCCCCCTAAGATCAACGAGAGGCTGAGAGAGACTTACCTTGTGTCTCAG	850

Db 493 GACTGATACCTTTTCCGAGTCACTGTAAGGCGGAGAAAGCTTACCTCCGTGGCTTCGG 552  
 Qy 851 AAATCATGATGTACATCCCTCTGGTCTTCTCTCAACCCTGTGGCTCTCATCGAGATGATAT 910  
 Db 553 AAATCATGATGTACATCCCTCTGGTCTTCTCTCAACCTGTGGCTGTATTATGATGATATCT 612  
 Qy 911 ATTGCTACAGAAAGCTCTCAAAAGCCGAAAGGAGAGCCCAAGAAAGCGCTGTGACTATACC 970  
 Db 613 ATTGCTACAGAAAGCTCTTAAAGCCGAAAGGCGAGACAGAAAGGCGTGTACTATACC 672  
 Qy 971 TTGCTATCCCATCTGAGAACAGAGAGAACTCTGCGGTACAGTGTAGAGAAATAGAAACAGA 1030  
 Db 673 TTGCTATCCCTTTCAGAGAAACAGAGAAACTCTGTGTATACCTGTGTGAGAGAAATA-----AT 726  
 Qy 1031 GCAGTGTGACATGAGGTGGCCCTGAAACACTGAGGGACTGACATCCCATGTTTCAGCAATG 1090  
 Db 727 GTGTGTGTGACTTGTGAGTGAATCTG-AGTGCTGAGGAGATCTGATATATCCCAAGTTCAGTATG 785  
 Qy 1091 TCATGTGATAGAGAGGGGCGCCCAAGGGCCCATGCGTTCCCTTCATGTGATTCAT 1146  
 Db 786 CCACCAATATTCAGGAAGTGGCCCAAGGTGTCCCAACAATCCATCTTTTCTATTTAT 841

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RESULT 4
US-09-977-579-3
: Sequence 3, Application US/09977579
: Publication No. US20040248240A1
:
: GENERAL INFORMATION:
: APPLICANT: Cambridge University Technical Services
: TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
: TITLE OF INVENTION: channel
: TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses th
: FILE REFERENCE: 674558-2001
: CURRENT APPLICATION NUMBER: US/09/977,579
: CURRENT FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: PCT/EP00/01783
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: 60,129,473
: PRIOR FILING DATE: 2000-02-24
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: PatentIn version 3.1
:
: SEQ ID NO 3
:
: LENGTH: 2220
:
: TYPE: DNA
:
: ORGANISM: rat
:
: US-09-977-579-3

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Query Match	42.8%	Score 540;	DB 11;	Length 2220;
Best Local Similarity	89.3%	Pred. No. 3.7e-157;		
Matches 582;	Conservative	0;	Mismatches 70;	Indels 0;
				Gaps 0;

Oy	371	GAAGATGCCGCTTCAATGATTTGTTCCCGGCGTTCTGTCTTATCTACGGG	430
Db	358	AAAGATGCCGCTTCAACGATTTGCTCCCTAGCTTCTTAGTGCTACTACGGG	417
Oy	431	TCAGTGTCTTCCCTGTGTGTGTGAGATGCCCTTGGAGACGGAGCGCTGACGGCA	490
Db	418	TCAAGTCTGTTCCCTGTGTGTGTGAGAGGCGCTTGGAGACGAACGGTGTGAGGGCA	477
Oy	491	ACCCCATGAAGCTGCGTGCAATCTCCGTCATGAGAGAGAGAGATGAGGCCACCA	550
Db	478	ATCCCATGAAGCTAGGTGCAATCTCTGTGCATGAAGAGAGAGATGAGGCCACCA	537
Oy	551	TGTTGGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTTCTTATTTTACGATATGGA	610
Db	538	TGTTGGAATGTTCTACAGGCCCTGAGGGCGGTAAAGATTTTCTTATTTATGATATCGA	597
Oy	611	ATGGCCACCAAGGAGTGGAGAGCCCTTTACAGGGGCGCTGCAATGGAATGGACCAAGG	670
Db	598	ATGGCCACCAAGGAGTGGAGAGCCCTTTCCAGGCGCTTGTCAATGGAATGGAGCAAGG	657
Oy	671	ACCTGACGAGCGTGTCCATCATCTGTGTCTCAACGTCACTCTGAACGACTCTGGCCTTACA	730

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Db 658 ACCTCAGAGACCTATCCATCACTGTAATCACTTGAATCACTCGCCCTTACA 717
Qy 721 CCGAATGTCGCCGGAGTTGAGTTGAGGCGATCGCCCTTTGGAAGAGAGCGC 790
Db 718 CATTGAATGTCGAGGAGTTGCAATTCAGGACACAGGCGCTTTGGAAGACACGA 777
Qy 721 GCGTATCCCCCTAAGAGTCAACGAGAGCTGAGAGACTTCACTCTGTGTCTAG 850
Db 778 GACTATACCTTTGGAGTCACTGAAGAGCGGGAAGAACTTCACTCGTGTCTAG 837
Qy 851 AATCATGATGTAATCTCTGTGTCTCTCACTCGTGTGTCTCATCGATGATAT 910
Db 838 AATCATGATGTAATCTCTGTGTCTCTCACTCGTGTGTCTCATCGATGATAT 897
Qy 911 ATTGCTACGAAAGGCTCAAAAGCGGAAGAGAGCGCCCAAGAAAGCGCTGACTAC 970
Db 898 ATTGCTACGAAAGGCTCTTAAGCGGAAGAGAGAGCAAGAAATGCGTGTGACTAC 957
Qy 971 TTGCAATCCCATCTGAGAACAGAGAACTCTGCGTACAGTGTGAGAGATA 1022
Db 958 TTGCAATCCCTTCAAGAAACAGAGAACTCTGTGTGACTGTGAGAGATA 1009
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RESULT 5
US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21
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Query Match 42.4%; Score 534.6; DB 13; Length 645;
Best Local Similarity 89.3%; Pred. No. 1.1e-155;
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 376 ATGCTGCTTCAATAGATGTTTCCCTGCTTCTCTGCTTATCTACGAGTCACT 435
Db 1 ATGCTGCTTCAATAGATGTTTCCCTGCTTCTCTGCTTATCTACGAGTCACT 60
Qy 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTGAGAGAGAGCGCTGAGAGCAACCC 495
Db 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTGAGAGAGAGCGCTGAGAGCAACCC 120
Qy 496 ATGAAGCTGCGTGTGATCTCTGATGAAGAGAGAGAGTGTGAGCAACCGTGTG 555
Db 121 ATGAAGCTGAGGTGATCTCTGATGAAGAGAGAGAGTGTGAGCAACCGTGTG 180
Qy 556 GAATGCTTCTACAGCCCGGAGGCGGTAAAGTTCTTATTTACGATATGCAATGC 615
Db 181 GATGCTTCTACAGCCCGGAGGCGGTAAAGTTCTTATTTACGATATGCAATGC 240
Qy 616 CACCGAGAGTGAAGAGCCCTTTAGGAGCGCTGAGTGAATGAGAGAGAGAGCTG 675
Db 241 CACCGAGAGTGAAGAGCCCTTTAGGAGCGCTGAGTGAATGAGAGAGAGAGCTG 300
Qy 676 CAGAGCTGTCCATCACTGTGTCTCAAGCTCACTGAAAGACTGTGAGCTTACCTGC 735
Db 676 CAGAGCTGTCCATCACTGTGTCTCAAGCTCACTGAAAGACTGTGAGCTTACCTGC 735
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Db 301 CAGAGCTATCATCACTGTAATGTCATTTGAATGACTCTGCGCTTACATGCG 360
Qy 726 AATGTCGCCGAGATTGAGTTGAGGCGCATCGGCCCTTTGTAAGACAGAGCGCTG 795
Db 361 AATGTCGCCGAGATTGAGTTGAGGCGCATCGGCCCTTTGTAAGACAGAGACTG 420
Qy 796 ATCCCTTGAAGTCAACGAGAGAGCTGAGAGAACTTCACTCTGTGTGTCTGAAATC 855
Db 421 ATACCTTTGCAAGTCACTGAAGAGCGGAGAGAACTTCACTCGTGTGTCTGAAATC 480
Qy 856 ATGATGTAATCTCTGTGTGTCTCTCACTCTGTGTGTGTCTCATGATATATATGC 915
Db 481 ATGATGTAATCTCTGTGTGTCTCTCACTCTGTGTGTGTGTATGATGATATATGC 540
Qy 916 TACAGAAAGTCTCAAAAGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 975
Db 541 TACAGAAAGTCTCTAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 976 ATCCCATCTGAGAACAGAGAGAACTCTGCGGTACAGTGTGAGAGAA 1020
Db 601 ATCCCTTCAAGAAACAGAGAGAACTCTGTGTGACTGTGTGAGAGAA 645
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RESULT 6
US-09-764-891-7659
; Sequence 7659, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN ET AL.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7659
; LENGTH: 4625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7659
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Query Match 17.1%; Score 216; DB 10; Length 4625;
Best Local Similarity 100.0%; Pred. No. 3.9e-56;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1044 AGTGGCTTGAACACCTGAGGAGTGCATCCCATGTTGCAATGTCATGCGATCAG 1103
Db 33 AGTGGCTTGAACACCTGAGGAGTGCATCCCATGTTGCAATGTCATGCGATCAG 92
Qy 1104 GAGGCGGCCCAAGGCGCCCATCGCTTCCCTTCAATGATCATGTTGTTCAATTATT 1163
Db 93 GAGGCGGCCCAAGGCGCCCATCGCTTCCCTTCAATGATCATGTTGTTCAATTATT 152
Qy 1164 CATCATATCATCACTGCTCTGAGCTTTTCACTCTGATCTCCCTAATCTCATGAGCT 1223
Db 153 CATCATATCATCACTGCTCTGAGCTTTTCACTCTGATCTCCCTAATCTCATGAGCT 212
Qy 1224 CTACGACCATTAAGACTCTGCGAAGACTGTGAGAGCC 1259
Db 213 CTACGACCATTAAGACTCTGCGAAGACTGTGAGAGCC 248
```

```
RESULT 7
US-10-029-191-23
; Sequence 23, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
```

```

:
: CURRENT FILING DATE: 2001-12-20
:
: PRIOR APPLICATION NUMBER: 09/569,978
:
: PRIOR FILING DATE: 2000-05-12
:
: PRIOR APPLICATION NUMBER: US 60/134,198
:
: PRIOR FILING DATE: 1999-05-14
:
: NUMBER OF SEQ ID NOS: 23
:
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO: 23
:
: LENGTH: 657
:
: TYPE: DNA
:
: ORGANISM: Lepus Sp.
:
: US-10-029-191-23

```

Query Match	11.8%	Score 148.2	DB 13	Length 657
Best Local Similarity	77.7%	Pred. No. 2.6e-35		
Matches 333	Conservative	0	Mismatches 223	Indels 21
				Gaps 3

QY	451	TGTGTGAAAGTGCCTCTCGGAGACGAGAGCGCGTGCAGAGGGCAACCCCAATGAAGCTGCCTGC	510
Db	61	TGCGTGGAGGTGAGCTTCGGAGACCAGAGCCGTGTACGGAGTGCCTTCAAAATTTCTGTGC	120
QY	511	ATCTCTCATGTAAAGAGAGAGGAGGTGAGAGCCACCAGGTGTGAAATGTGTTCTACAG	570
Db	121	ATCTCTCTCAAGCGCGCGACGACAGACACAGCGCGAGAACCTTCACGAATGTGACCTTCCGC	180
QY	571	CCCCGAGGCGGTAAAGATT-----TCTTATTACGATATCGAAATGGCCACAG	621
Db	181	CAGAAAGGCACATGAGAGAGTTTCGTCAAGATCTCGCGCTATAGAAACGAGGTGCTGCAGCTG	240
QY	622	GAGGTGAGAGAGCCCTTTCAAGGGGCGCCGCAATGGCAATGGCA-----CAAGGAC	672
Db	241	GAGGAAAGACAGCCCTTTGAGGCGCGCGTGTGTGAAACGACGCCGGGACACCAAGGAC	300
QY	673	CTGCAGACGTTGTCATCATCTGTGTCAACGTCACTCTGAACGACTCTGGCCTCTACACC	732
Db	301	CTGCAGACGCTGTCCATCTTTCATCAACCAATGTACCTTACACCACTCTGGCGACTACAG	360
QY	733	TGCAATGTGTCCCGGAGTTTGAAGTTGAAGCGCATCGGCCCTTTGTAAAGACGACGCG	792
Db	361	TGCCATGTCTACCGCGCTGCTCTCTTCGAAAATCAAGACACAAACACGAGCTGTCAAG	420
QY	793	CTGATCCCCCTAAAGATCACGAGAGAGGTGAGAGAGACTTCACTCTGTGTCTCAGAA	852
Db	421	AAGATCCACCTCGAGGTGTGTGACAAAGGCCAACAGAGCATGTGCATTCATCTGTGTGAG	480
QY	853	ATCATGATGATACATCTTCTGTGTTCTTCCACACCTGTGGCTGTCAATCGAGATGATATAT	912
Db	481	ATCATGATGTACGTCTCATCTGTGTGTGACCATCTGCTCTGTGGAGATGTGTAC	540
QY	913	TGCTACAGAAAGTCTCAAAAGCCGAGAGAGCA--GCCCAAGAAAACGCTGTGACTAC	969
Db	541	TGCTACAGAAAGATCGCGCGCCACCGAGAGGACGCGGCCAAGAGAACCGCTCGAATAC	600
QY	970	CTTGCGCATCCCATCTGAGAACAGAGAACTCTGCGG	1006
Db	601	TTGGCATTCACCTCAGAAAGCAAGAAATTCACG	637

RESULT 8  
 US-10-723-860-2247  
 Sequence 2247, Application US/10723860  
 Publication No. US20040253606A1  
 GENERAL INFORMATION:  
 APPLICANT: Aziz, Natsasha  
 APPLICANT: Ginsburg, Wendy M.  
 APPLICANT: Zlotnik, Albert  
 TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
 OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
 FILE REFERENCE: 05882.0193.NPUS01  
 CURRENT APPLICATION NUMBER: US/10/723.860  
 CURRENT FILING DATE: 2003-11-26  
 PRIOR APPLICATION NUMBER: 60/429,739  
 PRIOR FILING DATE: 2002-11-26

```

; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2247

```

Query Match	11.4%	Score 143.8; DB 18;	Length 1335;
Best Local Similarity	56.9%	Pred. No. 7.8e-34;	
Matches 334; Conservative	0;	Mismatches 232;	Indels 21; Gaps 3

[illegible]

```

RESULT 9
US-10-477-272-1
; Sequence 1, Application US/10477272
; Publication No. US20040191791A1
; GENERAL INFORMATION:
; APPLICANT: Biomedics Limited
; TITLE OF INVENTION: P12
; FILE REFERENCE: SCN1B (R85C)
; CURRENT APPLICATION NUMBER: US/10/477,272
; CURRENT FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-272-1

Query Match      11.3%; Score 142.2; DB 18; Length 1414
Beet Local Similarity 56.7%; Pred. No. 2.56-33;

```

	Matches	333; Conservative	0; Mismatches	233; Indels	21; Gaps	3
QY	441	CTTCCCTGTGTGTGGAAAGTCCCTCGGAGACGAGGCCGTGACGGGCAACCCCATGAA				500
Dp	151	CTGGCGGGGGCTGGCGTGGAGGTGAGATCGGAGACCGAGGCGCGTATGAGATGACCTTCAA				210
QY	501	GCTGGCTGCATCTCTCTCATGAAAGAGAGAGGTGAGAGCCACACCGTGTGTGAATG				560
Dp	211	AATCTTTGCATCTCTCTCGACAGCGCGCAGCGAGACCAAGCTGAGACCTTACCGAGTg				270
QY	561	GTTCTACAGGCCCCGAGGGCGGTAAAGTT-----TCTTATTTACGACTATCGGAA				611
Dp	271	GACCTTCCGACAGAAAGGGCACATGAGAGATTGTGTCAAGATCTCGCGTATGAGAAATGAGGT				330
QY	612	TGGCCACAGGAGGTGGAGAGGCCCTTTTCAGGGGGGCCCGACGTGGAAATGAGG-----				665
Dp	331	GTTGAGCTGGAGAGGAGATGAGTGTCTTGAGGGGCGCGTGTGTGAATGGACGCCGGGG				390
QY	666	---CAAGACCTGCAGAGACGTGTCCATCACTGTGCTCAACGTCACCTGAAAGCACTCTGG				722
Dp	391	CACCAAAABACTGGACAGATCTGTCTATCTTATCAACACATATGTCACCTTCAACAACACTCGGG				450
QY	723	CCTTCAACCTGCAAATGTGTCCCGGAGATTGAGTTGAAGCGCATCGGCCCTTTGTGAA				782
Dp	451	CGACTACAGATGCCACGCTCTACCGCGTGTCTTCTTCGAAACCTGACGACCAACACACG				510
QY	783	GACGACGGGGCTGATCCCCCTTAAAGTCAACGAGGAGGTGAGAGGATTCAACCTGTGT				842
Dp	511	CGTCGCTCAAGAGATTCACATTTGAGGTAGTGGACAAAGCCAAACAGAGATGGCATTCAT				570
QY	843	GGTCTCAGAAATCATGATGTATCATCTCTTGTGTTCTTCTCAACCTGTGGCTGTCAATGCA				902
Dp	571	CGTGTCTGAGATCATGATGTATGTGCTCATTTGTGGTGTGACCAATATGGCTGTGGCAGA				630
QY	903	GATGATATATTGCTTACAGAAAGGTCTCAAAAGCCGGAAG---GCAAGCCCAAGAAAAGCC				959
Dp	631	GATGATTTACTGCTTCAAGAAAGATGCTGCGCCGCAACGAGATGCTGTCACAGAGAAATGC				690
QY	960	GCTGTACTACTTGGCATCCATCTGAGAACAAAGAGAACTGTGGCG 1006				
Dp	691	CTCGGAATACTGGCCATCTACTCTTGAAAGCAAAAGAACTGCACGG 737				

```

RESULT 10
US-10-276-718/c
; Sequence 718, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y., Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 718
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-718

Query Match      11.2%; Score 141; DB 17; Length 407;
Best Local Similarity 96.6%; Pred. No. 3,8e-33;
Matches 144; Conservative 0; Mismatches 5; Indels 0; Gaps 0

Oy      820 GGTGAGAGGAGCTTCACCCCTGTGGCTTCAGAAATCATGATGACATCCTTCGTGGCTTC      879
Db      230 GGTGAGAGGAGACTTCACCTCTGTGGCTTCAGAAATCATGATGACATCCTTCGTGGCTTC      171

```

Qy	880	CTACCCCTGGGCGCTGCATCGAGATATATATATGTCATACAGAAAGGCTCTCAAAAGCCGAA	939
Db	170	CTACCTTGTGGCTGCTCATCGAGATATATATTGCTACAGAAAGTCTCAAAAGCCGAA	111
Qy	940	GAGGACGCCCAAGAAAAGCGCTGTGACTA	968
Db	110	GAGGACGCCCAAGAAAAGCGGTATGCTCA	82

RESULT 11  
US-09-917-800A-1654  
; Sequence 1654, Application US/09917800A  
; Patent No. US20020119462A1  
GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Castile, Arthur  
; APPLICANT: Elashoff, Michael  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5038-US  
; CURRENT APPLICATION NUMBER: US/09/917,800A  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,040  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,880  
; PRIOR FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: US 60/290,029  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/290,645  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: US 60/292,336  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/295,798  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/297,457  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,884  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,459  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 1740  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1654  
; LENGTH: 1490  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM\_017288  
US-09-917-800A-1654

Query Match	11.0%;	Score 138.6;	DB 9;	Length 1490;
Best Local Similarity	56.7%;	Pred. No. 3.4e-32;		
Matches 327;	Conservative 0;	Mismatches 229;	Indels 21;	Gaps 3;

Qy	451	TGTGTGGAAGGACCCCTTCGAGACGAGAGCGCGTCGACAGGGCAACCCCATGAACTGCGGTGC	510
Db	280	TGCGTGAAGGTGATTTCTGAGACCGAGGCACTGATATGAGATGACCTTCAAAATCTGTGT	339
Qy	511	ATCTCTTCGATGAAGAGAGAGAGAGGTGAGGCCACACCGGTGTGTAATGGTTCTACAG	570
Db	340	ATCTCTGTAAAGCTGTGATGAGACACCGCGAGACCTTCACGAGTGGACCTTCCGC	399
Qy	571	CCCGAGGCGGTAAAGATT-----TCTTATTTTACAGATATCGGAATGGCAACAG	621
Db	400	CAGAAAGGCACAGAGGAATTTGTCAAGATCTTACGCTATGAGATGAGATGGTCTGCACCTG	459
Qy	622	GAGGTGAGAGACCCCTTTCAGGGGCGCGCTGACGTGAATGGACAG-----CAAGAC	672
Db	460	GAGGAAGATGAGCCCTTTGAGGGCGCGTGTGTGTGGAACGTATATCGGGGACCAAGAC	519

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RESULT 11
US-09-917-800A-1654
; Sequence 1654, Application US/09917800A
; Patent No. US20020119462A1
GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Blashoff, Michael
; APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1654
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017288
US-09-917-800A-1654

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Query Match	11.0%;	Score 138.6;	DB 9;	Length 1490;
Best Local Similarity	56.7%;	Pred. No. 3.4e-32;		
Matches 327;	Conservative	0;	Mismatches 229;	Indels 21;
				Gaps 3;

OY	511	ATCTCTTGATGAAGAGAGAGAGTGGAGGCCACACGGTGTGGAAATGGTTCTACAGG	570
Db	280	TGCGTGGAGGTGGATTCTGAGACCGAGGCACTGATATGGATGACCTTCAAAATCTGTGT	339
OY	451	TGTTGGAAAGTGCCTCGAGAGACGAGAGCGCTGACAGGGCAACCCCATGAAGCTGCGCTGC	510
OY	622	GAGGTGGAGAGCCCTTTCAAGGGCGCGCTGACGTAGGAATGGCCAG-----CAAGAC	672
Db	460	GAGGAAAGTGAAGCCCTTGAAGGGCCGCTGTGTGGAAACGTATCTCGGGACCAAGAC	519
OY	571	CCCGAGGGCGGTAAAGATT-----TCTTATTTTACAGATATCGGAATGGCCACACG	621
Db	400	CAGAAAGGCACAGAGGAATTTGTCAAGATCTCTACGCTATGAGATGAATGAAGTGCTGCGACCTG	459





FEATURE:  
; OTHER INFORMATION: MAP TO CHR19.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2  
; OTHER INFORMATION: SWISSPROT HIT: Q07699, EVALUE 5.00e-42  
; OTHER INFORMATION: NT HIT: U12191.1, EVALUE 0.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: BF953777.1, EVALUE 1.00e-129  
US-10-029-386-16214

Query Match 3.9%; Score 49; DB 16; Length 243;  
Best Local Similarity 60.1%; Pred. No. 0.00014;  
Matches 104; Conservative 0; Mismatches 60; Indels 9; Gaps 1;

QY 598 TACGAGTATCGGATGCGCCAGCAGAGTGAGAGCCCTTTCAGAGGGCGCTGCAGTGG 657  
DB 4 TATGAGATGAGCTGTGACGTGAGGAGATGAGCCGCTTCAGAGGGCGCGTGGTGG 63  
QY 658 AATGGCAG-----CAGGACCTGCGAGCGTGTCCATCATGTGCTCAACGCTCACT 708  
DB 64 AATGGCAGCGGGGCGACCAAGACCTGCGAGATCTGTCTATCTTCATCACCAATGTCAAC 123  
QY 709 CTGAACGACTGTGGCTGTACACCTGCATGTGTCGCCGGAGTTGAGTTGA 761  
DB 124 TACAACCACTGGGGGACCTACAGATGCACGTCCTACCGCTCTCTTTCGA 176

## RESULT 15

US-10-029-386-2514  
; Sequence 2514, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
; FILE REFERENCE: AEWICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029.386  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 2514  
; LENGTH: 569  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR19.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2  
; OTHER INFORMATION: SWISSPROT HIT: Q07699, EVALUE 6.00e-42  
; OTHER INFORMATION: NT HIT: U12191.1, EVALUE 0.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: B1754689.1, EVALUE 0.00e+00  
US-10-029-386-2514

Query Match 3.9%; Score 49; DB 16; Length 569;  
Best Local Similarity 60.1%; Pred. No. 0.00019;  
Matches 104; Conservative 0; Mismatches 60; Indels 9; Gaps 1;

QY 598 TACGAGTATCGGATGCGCCAGCAGAGTGAGAGCCCTTTCAGAGGGCGCTGCAGTGG 657  
DB 62 TATGAGATGAGCTGTGACGTGAGGAGATGAGCCGCTTCAGAGGGCGCGTGGTGG 121  
QY 658 AATGGCAG-----CAGGACCTGCGAGCGTGTCCATCATGTGCTCAACGCTCACT 708

DB 122 AATGGCAGCGGGGCGACCAAGACCTGCGAGATCTGTCTATCTTCATCACCAATGTCAAC 181  
QY 709 CTGAACGACTGTGGCTGTACACCTGCATGTGTCGCCGGAGTTGAGTTGA 761  
DB 182 TACAACCACTGGGGGACCTACAGATGCACGTCCTACCGCTCTCTTTCGA 234

Search completed: April 1, 2005, 23:48:30  
Job time : 823 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 18:32:30 ; Search time 4595 Seconds  
(without alignments)  
10445.929 Million cell updates/sec

Title: US-09-977-579-4

Sequence: 1 cccctccctccgcagctgagc.....tgccagactgagagcccg 1261

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1252.2	99.3	4052	3	HSMB01563
2	909.4	72.1	2555	3	CR609664
3	768.6	61.0	1062	3	EX420015
4	652.6	51.8	975	5	EX445002
5	646.4	51.3	648	9	AY419145
6	574	45.5	582	5	BP202832
7	567.8	45.0	582	5	BP200910
8	550.6	43.7	1259	3	AK076466
9	542.6	43.0	3549	3	AK049747
10	536.6	42.6	648	9	AY419147
11	531.6	42.2	4149	3	AK049286
12	524.4	41.6	672	2	BB614118
13	521.4	41.3	636	5	BM933157
14	514.2	40.8	4105	3	BC058083
15	513	40.7	1078	1	AL534136
16	486.4	38.6	584	5	BP361278
17	473.6	37.6	950	4	BG294174
18	465	36.9	584	9	AY419146
19	453.2	35.9	723	6	CA749311
20	447.2	35.5	927	5	BQ713131
21	420.8	33.4	582	5	BP311484
22	397.4	31.5	1069	5	BM928131
23	390.8	31.0	825	5	BQ745919
24	386.4	30.6	846	6	CD355879

25	363.4	28.8	742	6	CB526211	CB526211	UI-M-PY0-
26	354	28.1	845	6	CA327438	CA327438	UI-M-PY0-
27	352.8	28.0	986	5	BUI18914	BUI18914	603142291
28	349.2	27.7	700	4	BT739617	BT739617	603361873
29	348	27.6	975	5	EX452112	EX452112	EX452112
30	347	27.5	692	7	CN219870	CN219870	WLA010B08
31	341.8	27.1	652	2	BB652801	BB652801	BB652801
32	332.4	26.4	892	5	BU368614	BU368614	603790206
33	326.4	25.9	595	5	BU368531	BU368531	603788820
34	310	24.6	450	6	CB787935	CB787935	AMGNNUC:N
35	307.2	24.4	712	6	CB526257	CB526257	UI-M-PY0-
36	306.2	24.3	734	7	CK367344	CK367344	AGENCOURT
37	305.2	24.2	780	5	BO770528	BO770528	UI-M-PY0-
38	303.6	24.1	823	7	CO428866	CO428866	UI-M-PY0-
39	297.2	23.6	750	6	CD349206	CD349206	UI-M-PY0-
40	294.2	23.3	895	5	EX743834	EX743834	EX743834
41	287.2	22.8	714	7	CF531573	CF531573	UI-M-PY0-
42	273.4	21.7	669	5	BM951151	BM951151	UI-M-PY0-
43	269.8	21.4	471	6	CB732717	CB732717	AMGNNUC:N
44	264.4	21.0	705	6	CD349958	CD349958	UI-M-PY0-
45	256.8	20.4	798	7	CF290312	CF290312	AGENCOURT

#### ALIGNMENTS

RESULT 1  
LOCUS HSMB01563  
DEFINITION Homo sapiens mRNA, CDNA DKFZp761F182 (from clone DKFZp761F182).  
ACCESSION AL136589  
VERSION AL136589.1 GI:13276680  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 4052)  
Ottewaelde, B., Obermaier, B., Deutschenbur, S., Schaipe, A.,  
Mewes, H.W., Weill, B., Amid, C., Osaenger, A., Fodor, G., Han, M. and  
Wiemann, S.  
The German CDNA Consortium  
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr. 1, D-85764  
Neuerberg, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Medigenomix (Martinsried/Germany) within the CDNA  
sequencing consortium of the German Genome Project.  
This clone (DKFZp761F182) is available at the RZPD Deutsches  
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp761F182  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

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## ORIGIN

Query Match	99.3%	Score 1252.2	DB 3	Length 4052
Best Local Similarity	99.8%	Pred. No. 0		
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				Gaps 0

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QY	63	GCTGGAGTTCCGGGGTGGGCGGGAGGCGAGCTGTCCGTGTGTCTGAGCGCGGCGAGAGC	122
Dp	491	GCTGGAGTTCCGGGGTGGGCGGGAGGCGAGCTGTCCGTGTGTCTGAGCGCGGCGAGAGC	550
QY	123	GGGGCGGGAGGGGCGTATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGGTTCGTTAAGG	182
Dp	551	GGGGCGGGAGGGGCGTATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGGTTCGTTAAGG	610
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Dp	611	CCCAAAGCCCCCACCAGCTCCAAAAGCTCCAGGGGCTCCCAAGGACCGAGTGTCCGAC	670
QY	243	CCTTCCTTCGGTCAAGAAAGTGGCCCCCTGGGGGAGTTTCGTCCCAAAGGGTTTCCTGAA	302
Dp	671	CCTTCCTTCGGTCAAGAAAGTGGCCCCCTGGGGGAGTTTCGTCCCAAAGGGTTTCCTGAA	730
QY	303	AGAACTTGAGAGGGGCGAGCTCTTGACCGAGGGAATCTCTGTGTACCTTGGAAAGCG	362
Dp	731	AGAACTTGAGAGGGGCGAGCTCTTGACCGAGGGAATCTCTGTGTACCTTGGAAAGCG	790
QY	363	CGAGCCCCAAGAGATGCTGCTTCATATAGATTGTTTCCCTGGCTTCTCTGTGTCTTAT	422
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Dp	911	GCAAGGCAAAACCCATGAAGCTGCGCTGCATCTCCTGATGAAGAGAGAGAGGTGAGGC	970
QY	543	CACCAACGGTGTGAATGGTCTCTACAGGCCCGAGGGCGGTAAAGTTTCCTTATTAGA	602
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QY	723	CCTCTACACCTGCAATGTGTCCCGGGAAGTTTGAAGTGAAGGCGCATCGAGCCCTTGTGAA	782
Dp	1151	CCTCTACACCTGCAATGTGTCCCGGGAAGTTTGAAGTGAAGGCGCATCGAGCCCTTGTGAA	1210
QY	783	GACGACGGGCGTATCCCCCTTAAGAGTCAACGAGGAGCGTGAAGAGACTTCACTCTGT	842
Dp	1211	GACGACGGGCGTATCCCCCTTAAGAGTCAACGAGGAGCGTGAAGAGACTTCACTCTGT	1270
QY	843	GCTCTCAAAATCATGATGTATATCTCTTCTGTCTTCTCTCAACCTGTGTGCTGTATATGA	902
Dp	1271	GCTCTCAAAATCATGATGTATATCTCTTGTCTTCTCTCAACCTGTGTGCTGTATATGA	1330

Qy	903	GATGATATATTTGCTACAGAAAGGTCATAAAGCGAAAGAGGCCCAAGAAACGGCTC	962
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Qy	963	TGACTTACCTTGCCATCCCATCTGTGAGAACAGAGAACTCTGCGGTACAGTGGAGATA	1022
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Qy	1143	CCATTGTTCTGTTCACTTCATTCCATTCATTCACCTGGGCTCTGAGCTTTCACCTGTGA	1202
Db	1571	CCATTGTTCTGTTCACTTCATTCCATTCACCTGGGCTCTGAGCTTTCACCTGTGA	1630
Qy	1203	CTCCCTTAAGTCATCAGACCTCTAAGAGACCATAGACTCTGCCAGAACTGAGAGCC	1259
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LOCUS	DEFINITION	CR609664	255 bp	full-length cDNA clone CS0DF023YA09 of Fetal brain of Homo sapiens (human).	HTC 21-JUN-2004
RESULT 2					
CR609664					

ACCESSION	CR609664
VERSION	CR609664.1
KEYWORDS	GI:50490471
SOURCE	HTC; CNSLT_cDNA.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Homo sapiens

**REFERENCE**  
**AUTHORS**  
**TITLE**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 2555)  
Li, W. B., Gruber, C., Jeejee, J. and Polayes, D.  
Full-length cDNA libraries and normalization

REFERENCE	JOURNAL	REMARK
1	Unpublished	Contact : Peng Liang Email : <a href="mailto:fliang@lifeitech.com">fliang@lifeitech.com</a> URL : <a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 2555)

**AUTHORS** Genoscope.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

COMMENT

BP 191 91006 EVRY cedex - FRANCE (E-mail: seestre@genoscope.cns.it  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primed  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES	Location/Qualifiers
source	1. .2555

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/plasmid="pCMVSPORT_6"

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Matches 910; Conservative	0	Mismatches 1	Indels 0
			Gaps 0

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| | | | |  
Db    208 AGCCTTGAAGCCCCGACGCCAGAAATGCCTTCCTCAATAGATTGTTCCTCCCTGGCT 267

QY	409	CTCTCGAGCTTATATACCTGGGTCAGTGCTTCCTCCGTGTGTGGAAATGACCTCG	468
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QY	469	GAGACGAGGCCGTGTGACGAGGCCAACCCCATGAAGCTGCGCTGCATCTCTGCATGAAGA	528
Db	328	GAGACGAGGCCGTGTGACGAGGCCAACCCCATGAAGCTGCGCTGCATCTCTGCATGAAGA	387
QY	529	GAGAGGTGTGAGGCCCAACCGTGGTGGAAATGGCTTCAAGGCCCGGAGGGCGGTAAAGT	588
Db	388	GAGAGGTGTGAGGCCCAACCGTGGTGGAAATGGCTTCAAGGCCCGGAGGGCGGTAAAGT	447
QY	589	TTCTCTTATTTACGAGTATCGAATGGCCACACGAGAGGTGTGAGAGCCCTTTTCAGGGCGC	648
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QY	649	CTGCAGTGGAAATGGACGACAGGACTGTGACGAGCGTGTCCATCACTGTGTCAAGTCACT	708
Db	508	CTGCAGTGGAAATGGACGACAGGACTGTGACGAGCGTGTCCATCACTGTGTCAAGTCACT	567
QY	709	CTGAACGACTCTGGGCTCTACACCTCGCAATGTATCCCGGAGATTGAGTTTAAAGCGCAT	768
Db	568	CTGAACGACTCTGGGCTCTACACCTCGCAATGTATCCCGGAGATTGAGTTTAAAGCGCAT	627
QY	769	CGGCCCTTTGTGAAGACGACGCGGCTGATCCCCCTTAAGAGTCACCGAGAGGCTGAAGAG	828
Db	628	CGGCCCTTTGTGAAGACGACGCGGCTGATCCCCCTTAAGAGTCACCGAGAGGCTGAAGAG	687
QY	829	GACTTCAACCTCTGTGGTCTCAGAAATCAATGAATGTACATCTTCTGTCTTCTCAACCTGT	888
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Db	928	GGAACATCCCATGTTTCAGCAATGTCAATGGCATCAGAGAGGCGGCCCAAGGCGCCCATGCG	987
QY	1129	TTCCCTTCATGCAATCCATTGTTCGTTCATTCATTCATTCATTCATTCATTCATTCATTCAT	1188
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QY	1189	GCTTTCACCTGTGAATCCCTTAATCTCCATCAGACCTTACGCAACCAATGAAGACTTGGCAGA	1248
Db	1048	GCTTTCACCTGTGAATCCCTTAATCTCCATCAGACCTTACGCAACCAATGAAGACTTGGCAGA	1107
QY	1249	ACTGAGAAAGCC 1259	
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RESULT	3
BX420015	
LOCUS	
DEFINITION	BX420015 Homo sapiens FETAL BRAIN Homo sapiens CDNA clone
ACCESSION	BX420015
VERSION	BX420015.2
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (baes 1 to 1062)	Li, W. B., Gruber, C., Jessee, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	On May 13, 2003 this sequence version replaced gi:3064673

Genoscope - Centre National de Séquençage  
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE  
Email: [seqre@genoscope.cns.fr](mailto:seqre@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primers  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 6147.r  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?b=CS0DF022A0A5Q1&c=6147.r>.

**FEATURES**

**SOURCE**

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**ORIGIN**

Query Match	61.0%	Score 768.6	DB 5	Length 1062
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Matches 797; Conservative	15	Mismatches 44	Indels 1	Gaps 1

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QY	529	GAGAGGTGAGAGGCGCACCGTGTGTGAATGTTCTACAGGCCCGGAGCGGCTAAAGAT	588
Db	387	GAGAGGTGAGAGGCGCACCGTGTGTGAATGTTCTACAGGCCCGGAGCGGCTAAAGAT	446
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Db	447	TTCCTTTATTTACGATATTCGGAATGCGACCAAGAGAGGTGAGAGGCCCTTTTCAAGGGGCGC	506
QY	649	CTGCAGTGAATGACAGCAAGGACTTGCAGAGCGTGTCCATCACTGTGCTCAACGTCACCT	708
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QY	709	CTGAACGACTTGGCCCTTCTACACTTGCATATGTGTCCGGGAGTTTGAATTTGAAGCGCAT	768
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QY	769	CGGCGCTTTTGAAGACGACGCGGCTATCCCCCTAAGATGACCCGAGAGAGGCTGGAAG	828
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QY 1009 CCAATGGAGGAATAGAACAGAGAGCGGTGACATGAGTGGCGCTTGAACACCTGAGAGGACT 1068  
DB 867 CCAGTGGAGGAATAGAACAGAGAGCGGTGACATGAGTGGCGCTTGAACACCTGAGAGGACT 926  
QY 1069 GGACATCCCATGTTGAGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128  
DB 927 GGACATCCCATGTTGAGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 985  
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RESULT 4  
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LOCUS BX445002 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
DEFINITION CSQDF023YA09 5-PRIME, mRNA sequence.

ACCESSION BX445002  
VERSION BX445002.2 GI:47009181

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 975)  
AUTHORS Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 15, 2003 this sequence version replaced gi:30782286.

Genoscope - Centre National de Sequencage  
Contact: Genoscope  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seq@genoscope.cns.fr; Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

This sequence belongs to sequence cluster 6147.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CSI1AF062E05QPl&c=6147.r.

FEATURES  
source location/Qualifiers

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was primed with a NotI-oligo (dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

ORIGIN  
Query Match 51.8%; Score 652.6; DB 5; Length 975;  
Best Local Similarity 97.5%; Pred. No. 2.1e-158;

Matches 666; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

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DB 208 AGCCTGGAGACCGGACAGCCCAAGAGATGCTGCTTCAATGATGTTTCCCTGCT 267  
QY 409 TCTCTGCTTATCTACTGAGTCACTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468  
DB 268 TCTCTGCTTATCTACTGAGTCACTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 327  
QY 469 GAGACGAGAGCGGCTGACAGGCACTCCCATGAAAGTGGCTGCTATCTCTCATGAAAGGA 528  
DB 328 GAGACGAGAGCGGCTGACAGGCACTCCCATGAAAGTGGCTGCTATCTCTCATGAAAGGA 387  
QY 529 GAGAGAGTGAAGGCGGACCAAGGAGTGAATGTTCTACAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588  
DB 388 GAGAGAGTGAAGGCGGACCAAGGAGTGAATGTTCTACAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447  
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DB 448 TTCTTTATTTACAGATATCGAATGAGCCACAGAGAGTGAAGGCTTTCAGGGGCGC 507  
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DB 508 CTGCACTGGAATGAGAGCAAGGACCTGCAAGAGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 567  
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DB 688 GACTTCACCTCTGCT 747  
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RESULT 5  
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LOCUS AY419145 Homo sapiens HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.

ACCESSION AY419145  
VERSION AY419145.1 GI:39775105

KEYWORDS GSS.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 648)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanendazum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.D., Smitsky, J.C.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 648)

AUTHORS	Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tenenbaum,D.M., Civeleto,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smirsky,J.D., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.
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Best Local Similarity	99.8%; Pred. No. 7.8e-157;
Matches 647; Conservative	0; Mismatches 1; Indels 0; Gaps 0
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Dy	436 GTCTGCTTCCCTGTGTGTGTGTGAAGTGCCCTTCGAGAAGGAGGCCCTGACGGCAACCCC 495
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Dy	496 ATGAAGCTGCGCTGCATCTCTCGCATGAAAGAGAAGAGAGTGGAGGCCACCACGGTGGT 555
Dd	121 ATGAAGCTGCGCTGCATCTCTCGCATGAAAGAGAAGAGAGTGGAGGCCACCACGGTGGT 180
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Dd	241 CACGAGAGGTGTGAGAGGCCCTTTGAGGGGCGCTTCAGATGGATGGACAAGAACCTG 300
Dy	676 CAGGACCTGTCCATCTACTGTGTCTCAAAGTCACTCTGAACGACTCTGGCTCTACACCTGC 735
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Dy	736 AATGTGTCCCGGAGTTGAGTTGAGGCGCATGGGCCCTTTGTGAAGCAAGCGGGCTG 795
Dd	361 AATGTGTCCCGGAGTTGAGTTGAGGCGCATGGGCCCTTTGTGAAGCAAGCGGGCTG 420
Dy	796 ATCCCCCTAAGAGTCAACGAGAGGCTGTGAGAGACTTCACTCTGTGGTCTCAAAAATC 855
Dd	421 ATCCCCCTAAGAGTCAACGAGAGGCTGTGAGAGACTTCACTCTGTGGTCTCAAAAATC 480
Dy	856 ATGATGTACATCTTGTGGTCTTCTCTCAACCTGTGGCTGTCTATGGAATGATATATTGC 915
Dd	481 ATGATGTACATCTTGTGGTCTTCTCTCAACCTGTGGCTGTCTATGGAATGATATATTGC 540
Dy	916 TACAGAAAGGTCTCAAAGCGAAGAGGCAAGCCCAAGAAAAAGCGCTGACATCACTTGGC 975
Dd	541 TACAGAAAGGTCTCAAAGCGAAGAGGCAAGCCCAAGAAAAAGCGCTGACATCACTTGGC 600
Dy	976 ATCCCATCTGAGAACAGAGAGAACTCTGCGTATCCAGTGGAGGAATAG 1023
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VERSION	BP020832.1	GI:52054220
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 582)	
TITLE	Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions	
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp.	
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QY	155 TGGGAGGTCCAGTGGGGTGCCTTAAGGGCCCAAGCCCGGCTCCAAAAGCTCC	214
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QY	335 GAATCTCTGTGTAGCTTGGAAAGCCGACGCGCCAGAAATGCTGCTTCAATAGAT	394
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QY	395 TGTTCCTCCCTGCTCTCGTGTCTTAATCTAGTGGGTCAAGTGTGCTTCCCTGTGTG	454
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QY	455 TGAAGTGTCCCTCGAGAGCGAGGCGGTGACGAGCAACCCATGAAAGTGTGCTGATCT	514
DB	361 TGAAGTGTCCCTCGAGAGCGAGGCGGTGACGAGCAACCCATGAAAGTGTGCTGATCT	420
QY	515 CCTGCATGAGAGAGAGAGGTGAGGCGCACACGCTGTGTGAATGCTTCAACAGCCCG	574
DB	421 CCTGCATGAGAGAGAGAGGTGAGGCGCACACGCTGTGTGAATGCTTCAACAGCCCG	480
QY	575 AGGCGGCTAAAGATTTCTCTTAATTAACGATGTGGAATGGCACACGAGGCTGAGAGCC	634
DB	481 AGGCGGCTAAAGATTTCTCTTAATTAACGATGTGGAATGGCACACGAGGCTGAGAGCC	540
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 DEFINITION AMR03894, mRNA sequence.  
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 VERSION BP200910.1 GI:52050356  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
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 REFERENCE 1 (bases 1 to 582)  
 Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,  
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.  
 Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 Genome Res. 14 (9), 1711-1718 (2004)  
 JOURNAL Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp.  
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 120 CTGGAGACGAGGCGCGTGCAGAGCAACCCATGAGCGGCTCATCTCTGATGAA 179  
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 LOCUS AK076466  
 DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched  
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 BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus  
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 ACCESSION AK076466  
 VERSION AK076466.1 GI:26345409  
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 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 JOURNAL 99279253  
 MEDLINE 10349636  
 PUBMED 10349636  
 REFERENCE 2  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 JOURNAL 20499374  
 MEDLINE 11042159  
 PUBMED 11042159  
 REFERENCE 3  
 Shibata,K., Itoh,M., Aizawa,K., Nageoka,S., Sasaki,N., Carninci,P.,  
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 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,  
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 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 JOURNAL 20530913  
 MEDLINE 11076861  
 PUBMED 11076861  
 REFERENCE 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 JOURNAL 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 JOURNAL 6 (bases 1 to 1359)  
 REFERENCE Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,  
 Arikawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,  
 Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,  
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 Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kono,H., Kouda,M.,  
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,  
 Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,  
 Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,  
 Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,  
 Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,  
 Tejima,Y., Toyota,T., Yamamura,T., Yamanaka,I., Yasunishi,A.,  
 Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
 Direct Submission  
 Submitted (16-APR-2002) Yoshida Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),



RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES  
source  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fanom.gsc.riken.jp/  
location/Qualifiers  
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# CDS

## ORIGIN

Query Match 43.7%; Score 550.6; DB 3; Length 1359;  
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Matches 604; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
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DB 73 GATTGTTTCCCTGCTTCTCTGCTTCTCTGCTTCTCTGCTTCTCTGCTTCTCTG 132  
QY 452 GTGTGAGAGTCCCTCGGAGACGAGGCGCTGCAAGGCAACCCCATGAGCTGCGTCA 511  
DB 133 GTGTGAGAGTCCCTCGGAGACGAGGCGCTGCAAGGCAATTCATGAACTGAGATGCA 192  
QY 512 TCTCCTGATGAGAGAGAGAGTGGAGGCAACGAGTGGATGTTCTTACAGGC 571  
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QY 572 CCGAGGCGGTAAAGATTTCTTATTATTCAGATTCGAAATGGCCACAGAGAGTGGAGA 631  
DB 253 CCGAGGCGGTAAAGATTTCTTATTATTCAGATTCGAAATGGCCACAGAGAGTGGAGA 312  
QY 632 GCGCCCTTTTCAGGGGCGCTGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 691  
DB 313 GCGCCCTTTTCAGGGGCGCTGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372  
QY 692 CTGTGCTCAAGCTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751  
DB 373 CTGTGCTCAAGCTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432  
QY 752 TTGAGATTGAGAGGAGCTGGGCGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 811  
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QY 812 CCGAGAGGCTGAG 871  
DB 493 CTGAGAGAGGCGGAG 552  
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QY 932 AAGCCGAG 991  
DB 613 AGCCCGAG 672  
QY 992 AGGAGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024  
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AK049747  
VERSION  
AK049747.1 GI:26340475  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Carninci, P. and Hayashizaki, Y.  
TITLE  
High-efficiency full-length cDNA cloning  
JOURNAL  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE  
99279253  
PUBMED  
10349636

REFERENCE  
AUTHORS  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL  
Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE  
20499374  
PUBMED  
11042159

REFERENCE  
AUTHORS  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakeguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.  
TITLE  
RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL  
Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE  
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PUBMED  
11076861

REFERENCE  
AUTHORS  
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE  
Functional annotation of a full-length mouse cDNA collection  
JOURNAL  
Nature 409, 685-690 (2001)  
MEDLINE  
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PUBMED  
11076861

REFERENCE  
AUTHORS  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL  
Nature 420, 563-573 (2002)  
MEDLINE  
12053091  
PUBMED  
12053091  
REFERENCE  
AUTHORS  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,



Best Local Similarity 89.3%; Pred. No. 2,8e-128;  
Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog (Rattus norvegicus), full insert sequence.  
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VERSION AK049286.1  
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ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PubMed 10349636  
REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PubMed 11042159  
REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PubMed 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6  
AUTHORS (bases 1 to 4149)  
ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONO, H., CARNINCI, P.,  
FUKUDA, S., FURUKAWA, M., HANAGAKI, T., HARA, A., HASHIZUME, W.,  
HAYASHIDA, K., HAYATSU, N., HIRAMOTO, K., HIRAKAWA, T., HIRAZAKI, T.,  
HORI, F., IMOTO, K., ISHII, Y., ITOH, M., KAGAWA, I., KANAKAWA, T.,  
KATO, H., KAWAI, J., KOJIMA, Y., KONO, S., KONO, H., KODA, M.,  
KOYA, S., KURIHARA, C., MATSUYAMA, T., MIYAZAKI, A., MURATA, M.,  
NAKAMURA, M., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OHSAKI, N.,  
OKAZAKI, Y., SAITO, R., SAITOH, H., SAKAI, C., SAKAI, K., SAKAZUME, N.,  
SANO, H., SASEKI, D., SHIBATA, K., SHINAGAWA, A., SHIRAKI, T.,  
SOGABE, Y., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKAKU-KAHARA, S.,  
TAKEDA, Y., TANAKA, T., TOMARU, A., TOYA, T., YASUNISHI, A.,  
MURAMATSU, M., and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.  
Location/Qualifiers  
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			Mus musculus sodium channel, voltage-gated, type III, beta, mRNA (cDNA clone IMAGE:6826414), containing frame-shift errors.

VERSION	BC058083.1	GI:34784518
KEYWORDS	HTC.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE  
1 (bases 1 to 4105)  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

**TITLE** Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

**TITLE** Direct Submission  
**JOURNAL** Submitted (08-Sep-2003) National Institutes of Health, Mammalian

REMARK	COMMENT
NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	Contact: MGC help desk

Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLIL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@bcsc.bc.ca  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susama Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Leticia Hsiao, Martin Krzyzinski, Reta Kutsche, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Matheson, Candice Mcleavy, Steven  
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline  
Schein, Duane Smalue, Michael Smith, Lorraine Spence, Jeff Scott,  
Michael Thorne, Miranada Tsai, Natsuya Van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNLIL at: <http://image.lnl.gov>  
Series: IRMX Prime: 126 Row: 1 Column: 19  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 23943798  
This clone has the following problem: frame shifted.

Location/Qualifiers  
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FEATURES  
source

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Qy	656	GGATGGACAGCAAGACCTGCAAGACGTGTCCATCACTGTGCTCAACGTTCACTCTGAACG	71.5
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 1078)  
 Lj.W.B., Gruber,C., Jessee,J. and Polayes,D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 13, 2001 this sequence version replaced gi:30539643.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
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 This sequence belongs to sequence cluster 6147.r  
 For more information about this cluster, see  
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 enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

## FEATURES

source

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 vector. Library was not normalized."

## ORIGIN

Query Match 40.7%; Score 513; DB 1; Length 1078;  
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